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(54) Title: NOVEL COMPOUNDS

(57) Abstract: Polypeptides and polynucleotides of the genes set forth in Table I and methods for producing such polypeptides by recombinant techniques are disclosed. Also disclosed are methods for utilizing polypeptides and polynucleotides of the genes set forth in Table I in diagnostic assays.

Novel Compounds

Field of Invention

This invention relates to newly identified polypeptides and polynucleotides encoding such polypeptides, to their use in diagnosis and in identifying compounds that may be agonists, antagonists that are potentially useful in therapy, and to production of such polypeptides and polynucleotides. The polynucleotides and polypeptides of the present invention also relate to proteins with signal sequences which allow them to be secreted extracellularly or membrane-associated (hereinafter often referred collectively as secreted proteins or secreted polypeptides).

Background of the Invention

The drug discovery process is currently undergoing a fundamental revolution as it embraces "functional genomics", that is, high throughput genome- or gene-based biology. This approach as a means to identify genes and gene products as therapeutic targets is rapidly superseding earlier approaches based on "positional cloning". A phenotype, that is a biological function or genetic disease, would be identified and this would then be tracked back to the responsible gene, based on its genetic map position.

Functional genomics relies heavily on high-throughput DNA sequencing technologies and the various tools of bioinformatics to identify gene sequences of potential interest from the many molecular biology databases now available. There is a continuing need to identify and characterise further genes and their related polypeptides/proteins, as targets for drug discovery.

Proteins and polypeptides that are naturally secreted into blood, lymph and other body fluids, or secreted into the cellular membrane are of primary interest for pharmaceutical research and development. The reason for this interest is the relative ease to target protein therapeutics into their place of action (body fluids or the cellular membrane). The natural pathway for protein secretion into extracellular space is the endoplasmic reticulum in eukaryotes and the inner membrane in prokaryotes (Palade, 1975, Science, 189, 347; Milstein, Brownlee, Harrison, and Mathews, 1972, Nature New Biol., 239, 117; Blobel, and Dobberstein, 1975, J. Cell. Biol., 67, 835). On the other hand, there is no known natural pathway for exporting a protein from the exterior of the cells into the cytosol (with the exception of pinocytosis, a mechanism of snake venom toxin intrusion into cells). Therefore targeting protein therapeutics into cells poses extreme difficulties.

The secreted and membrane-associated proteins include but are not limited

to all peptide hormones and their receptors (including but not limited to insulin, growth hormones, chemokines, cytokines, neuropeptides, integrins, kallikreins, lamins, melanins, natriuretic hormones, neuropsin, neurotrophins, pituitary hormones, pleiotrophins, prostaglandins, secretogranins, selectins, thromboglobulins, thymosins), the breast and colon cancer gene products, leptin, the obesity gene protein and its receptors, serum albumin, superoxide dismutase, spliceosome proteins, 7TM (transmembrane) proteins also called as G-protein coupled receptors, immunoglobulins, several families of serine proteinases (including but not limited to proteins of the blood coagulation cascade, digestive enzymes), deoxyribonuclease I, etc.

Therapeutics based on secreted or membrane-associated proteins approved by FDA or foreign agencies include but are not limited to insulin, glucagon, growth hormone, chorionic gonadotropin, follicle stimulating hormone, luteinizing hormone, calcitonin, adrenocorticotrophic hormone (ACTH), vasopressin, interleukines, interferones, immunoglobulins, lactoferrin (diverse products marketed by several companies), tissue-type plasminogen activator (Alteplase by Genentech), hyaluronidase (Wydase by Wyeth-Ayerst), dornase alpha (Pulmozyme by Genentech), Chymodiactin (chymopapain by Knoll), alglucerase (Ceredase by Genzyme), streptokinase (Kabikinase by Pharmacia) (Streptase by Astra), etc. This indicates that secreted and membrane-associated proteins have an established, proven history as therapeutic targets. Clearly, there is a need for identification and characterization of further secreted and membrane-associated proteins which can play a role in preventing, ameliorating or correcting dysfunction or disease, including but not limited to diabetes, breast-, prostate-, colon cancer and other malignant tumors, hyper- and hypotension, obesity, bulimia, anorexia, growth abnormalities, asthma, manic depression, dementia, delirium, mental retardation, Huntington's disease, Tourette's syndrome, schizophrenia, growth, mental or sexual development disorders, and dysfunctions of the blood cascade system including those leading to stroke. The proteins of the present invention which include the signal sequences are also useful to further elucidate the mechanism of protein transport which at present is not entirely understood, and thus can be used as research tools.

Summary of the Invention

The present invention relates to particular polypeptides and polynucleotides of the genes set forth in Table I, including recombinant materials and methods for their production. Such polypeptides and polynucleotides are of interest in relation to methods of treatment of

certain diseases, including, but not limited to, the diseases set forth in Tables III and V, hereinafter referred to as "diseases of the invention". In a further aspect, the invention relates to methods for identifying agonists and antagonists (*e.g.*, inhibitors) using the materials provided by the invention, and treating conditions associated with imbalance of polypeptides and/or polynucleotides of the genes set forth in Table I with the identified compounds. In still a further aspect, the invention relates to diagnostic assays for detecting diseases associated with inappropriate activity or levels the genes set forth in Table I. Another aspect of the invention concerns a polynucleotide comprising any of the nucleotide sequences set forth in the Sequence Listing and a polypeptide comprising a polypeptide encoded by the nucleotide sequence. In another aspect, the invention relates to a polypeptide comprising any of the polypeptide sequences set forth in the Sequence Listing and recombinant materials and methods for their production. Another aspect of the invention relates to methods for using such polypeptides and polynucleotides. Such uses include the treatment of diseases, abnormalities and disorders (hereinafter simply referred to as diseases) caused by abnormal expression, production, function and or metabolism of the genes of this invention, and such diseases are readily apparent by those skilled in the art from the homology to other proteins disclosed for each attached sequence. In still another aspect, the invention relates to methods to identify agonists and antagonists using the materials provided by the invention, and treating conditions associated with the imbalance with the identified compounds. Yet another aspect of the invention relates to diagnostic assays for detecting diseases associated with inappropriate activity or levels of the secreted proteins of the present invention.

Description of the Invention

In a first aspect, the present invention relates to polypeptides the genes set forth in Table I. Such polypeptides include:

- (a) an isolated polypeptide encoded by a polynucleotide comprising a sequence set forth in the Sequence Listing, herein when referring to polynucleotides or polypeptides of the Sequence Listing, a reference is also made to the Sequence Listing referred to in the Sequence Listing;
- (b) an isolated polypeptide comprising a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
- (c) an isolated polypeptide comprising a polypeptide sequence set forth in the Sequence Listing;

- (d) an isolated polypeptide having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
- (e) a polypeptide sequence set forth in the Sequence Listing; and
- (f) an isolated polypeptide having or comprising a polypeptide sequence that has an Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polypeptide sequence set forth in the Sequence Listing;
- (g) fragments and variants of such polypeptides in (a) to (f).

Polypeptides of the present invention are believed to be members of the gene families set forth in Table II. They are therefore of therapeutic and diagnostic interest for the reasons set forth in Tables III and V. The biological properties of the polypeptides and polynucleotides of the genes set forth in Table I are hereinafter referred to as "the biological activity" of polypeptides and polynucleotides of the genes set forth in Table I. Preferably, a polypeptide of the present invention exhibits at least one biological activity of the genes set forth in Table I.

Polypeptides of the present invention also include variants of the aforementioned polypeptides, including all allelic forms and splice variants. Such polypeptides vary from the reference polypeptide by insertions, deletions, and substitutions that may be conservative or non-conservative, or any combination thereof. Particularly preferred variants are those in which several, for instance from 50 to 30, from 30 to 20, from 20 to 10, from 10 to 5, from 5 to 3, from 3 to 2, from 2 to 1 or 1 amino acids are inserted, substituted, or deleted, in any combination.

Preferred fragments of polypeptides of the present invention include an isolated polypeptide comprising an amino acid sequence having at least 30, 50 or 100 contiguous amino acids from an amino acid sequence set forth in the Sequence Listing, or an isolated polypeptide comprising an amino acid sequence having at least 30, 50 or 100 contiguous amino acids truncated or deleted from an amino acid sequence set forth in the Sequence Listing. Preferred fragments are biologically active fragments that mediate the biological activity of polypeptides and polynucleotides of the genes set forth in Table I, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Also preferred are those fragments that are antigenic or immunogenic in an animal, especially in a human.

Fragments of a polypeptide of the invention may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, these variants may be employed as intermediates for producing the full-length polypeptides of the invention. A polypeptide of the present invention may be in the form of the "mature" protein or may be a

part of a larger protein such as a precursor or a fusion protein. It is often advantageous to include an additional amino acid sequence that contains secretory or leader sequences, pro-sequences, sequences that aid in purification, for instance multiple histidine residues, or an additional sequence for stability during recombinant production.

- 5 Polypeptides of the present invention can be prepared in any suitable manner, for instance by isolation from naturally occurring sources, from genetically engineered host cells comprising expression systems (*vide infra*) or by chemical synthesis, using for instance automated peptide synthesizers, or a combination of such methods. Means for preparing such polypeptides are well understood in the art.
- 10 In a further aspect, the present invention relates to polynucleotides of the genes set forth in Table I. Such polynucleotides include:
- (a) an isolated polynucleotide comprising a polynucleotide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polynucleotide sequence set forth in the Sequence Listing;
 - 15 (b) an isolated polynucleotide comprising a polynucleotide set forth in the Sequence Listing;
 - (c) an isolated polynucleotide having at least 95%, 96%, 97%, 98%, or 99% identity to a polynucleotide set forth in the Sequence Listing;
 - (d) an isolated polynucleotide set forth in the Sequence Listing;
 - 20 (e) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
 - (f) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide set forth in the Sequence Listing;
 - 25 (g) an isolated polynucleotide having a polynucleotide sequence encoding a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
 - (h) an isolated polynucleotide encoding a polypeptide set forth in the Sequence Listing;
 - (i) an isolated polynucleotide having or comprising a polynucleotide sequence that has an
 - 30 Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polynucleotide sequence set forth in the Sequence Listing;
 - (j) an isolated polynucleotide having or comprising a polynucleotide sequence encoding a polypeptide sequence that has an Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polypeptide sequence set forth in the Sequence Listing; and

polynucleotides that are fragments and variants of the above mentioned polynucleotides or that are complementary to above mentioned polynucleotides, over the entire length thereof.

Preferred fragments of polynucleotides of the present invention include an isolated polynucleotide comprising an nucleotide sequence having at least 15, 30, 50 or 100
5 contiguous nucleotides from a sequence set forth in the Sequence Listing, or an isolated polynucleotide comprising a sequence having at least 30, 50 or 100 contiguous nucleotides truncated or deleted from a sequence set forth in the Sequence Listing.

Preferred variants of polynucleotides of the present invention include splice variants, allelic variants, and polymorphisms, including polynucleotides having one or more
10 single nucleotide polymorphisms (SNPs).

Polynucleotides of the present invention also include polynucleotides encoding polypeptide variants that comprise an amino acid sequence set forth in the Sequence Listing and in which several, for instance from 50 to 30, from 30 to 20, from 20 to 10, from 10 to 5, from 5 to 3, from 3 to 2, from 2 to 1 or 1 amino acid residues are substituted, deleted or
15 added, in any combination.

In a further aspect, the present invention provides polynucleotides that are RNA transcripts of the DNA sequences of the present invention. Accordingly, there is provided an RNA polynucleotide that:

(a) comprises an RNA transcript of the DNA sequence encoding a polypeptide set
20 forth in the Sequence Listing;

(b) is a RNA transcript of a DNA sequence encoding a polypeptide set forth in the Sequence Listing;

(c) comprises an RNA transcript of a DNA sequence set forth in the Sequence Listing; or

25 (d) is a RNA transcript of a DNA sequence set forth in the Sequence Listing; and RNA polynucleotides that are complementary thereto.

The polynucleotide sequences set forth in the Sequence Listing show homology with the polynucleotide sequences set forth in Table II. A polynucleotide sequence set forth in the Sequence Listing is a cDNA sequence that encodes a polypeptide set forth in the
30 Sequence Listing. A polynucleotide sequence encoding a polypeptide set forth in the Sequence Listing may be identical to a polypeptide encoding a sequence set forth in the Sequence Listing or it may be a sequence other than a sequence set forth in the Sequence Listing, which, as a result of the redundancy (degeneracy) of the genetic code, also encodes a polypeptide set forth in the Sequence Listing. A polypeptide of a sequence set forth in the
35 Sequence Listing is related to other proteins of the gene families set forth in Table II, having

homology and/or structural similarity with the polypeptides set forth in Table II. Preferred polypeptides and polynucleotides of the present invention are expected to have, *inter alia*, similar biological functions/properties to their homologous polypeptides and polynucleotides. Furthermore, preferred polypeptides and polynucleotides of the present invention have at least one activity of the genes set forth in Table I.

Polynucleotides of the present invention may be obtained using standard cloning and screening techniques from a cDNA library derived from mRNA from the tissues set forth in Table IV (see for instance, Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)). Polynucleotides of the invention can also be obtained from natural sources such as genomic DNA libraries or can be synthesized using well known and commercially available techniques.

When polynucleotides of the present invention are used for the recombinant production of polypeptides of the present invention, the polynucleotide may include the coding sequence for the mature polypeptide, by itself, or the coding sequence for the mature polypeptide in reading frame with other coding sequences, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro- protein sequence, or other fusion peptide portions. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain preferred embodiments of this aspect of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.*, Proc Natl Acad Sci USA (1989) 86:821-824, or is an HA tag. A polynucleotide may also contain non-coding 5' and 3' sequences, such as transcribed, non-translated sequences, splicing and polyadenylation signals, ribosome binding sites and sequences that stabilize mRNA.

Polynucleotides that are identical, or have sufficient identity to a polynucleotide sequence set forth in the Sequence Listing, may be used as hybridization probes for cDNA and genomic DNA or as primers for a nucleic acid amplification reaction (for instance, PCR). Such probes and primers may be used to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes (including genes encoding paralogs from human sources and orthologs and paralogs from other species) that have a high sequence similarity to sequences set forth in the Sequence Listing, typically at least 95% identity. Preferred probes and primers will generally comprise at least 15 nucleotides, preferably, at least 30 nucleotides and may have at least 50, if not at least 100 nucleotides. Particularly preferred probes will have between

30 and 50 nucleotides. Particularly preferred primers will have between 20 and 25 nucleotides.

A polynucleotide encoding a polypeptide of the present invention, including homologs from other species, may be obtained by a process comprising the steps of
5 screening a library under stringent hybridization conditions with a labeled probe having a sequence set forth in the Sequence Listing or a fragment thereof, preferably of at least 15 nucleotides; and isolating full-length cDNA and genomic clones containing the polynucleotide sequence set forth in the Sequence Listing. Such hybridization techniques are well known to the skilled artisan. Preferred stringent hybridization conditions include
10 overnight incubation at 42°C in a solution comprising: 50% formamide, 5xSSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10 % dextran sulfate, and 20 microgram/ml denatured, sheared salmon sperm DNA; followed by washing the filters in 0.1x SSC at about 65°C. Thus the present invention also includes isolated polynucleotides, preferably with a nucleotide sequence of at least 100,
15 obtained by screening a library under stringent hybridization conditions with a labeled probe having the sequence set forth in the Sequence Listing or a fragment thereof, preferably of at least 15 nucleotides.

The skilled artisan will appreciate that, in many cases, an isolated cDNA sequence will be incomplete, in that the region coding for the polypeptide does not extend all the way
20 through to the 5' terminus. This is a consequence of reverse transcriptase, an enzyme with inherently low "processivity" (a measure of the ability of the enzyme to remain attached to the template during the polymerisation reaction), failing to complete a DNA copy of the mRNA template during first strand cDNA synthesis.

There are several methods available and well known to those skilled in the art to
25 obtain full-length cDNAs, or extend short cDNAs, for example those based on the method of Rapid Amplification of cDNA ends (RACE) (see, for example, Frohman et al., Proc Nat Acad Sci USA 85, 8998-9002, 1988). Recent modifications of the technique, exemplified by the Marathon (trade mark) technology (Clontech Laboratories Inc.) for example, have significantly simplified the search for longer cDNAs. In the Marathon (trade mark)
30 technology, cDNAs have been prepared from mRNA extracted from a chosen tissue and an 'adaptor' sequence ligated onto each end. Nucleic acid amplification (PCR) is then carried out to amplify the "missing" 5' end of the cDNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated using 'nested' primers, that is, primers designed to anneal within the amplified product (typically an
35 adapter specific primer that anneals further 3' in the adaptor sequence and a gene specific

primer that anneals further 5' in the known gene sequence). The products of this reaction can then be analyzed by DNA sequencing and a full-length cDNA constructed either by joining the product directly to the existing cDNA to give a complete sequence, or carrying out a separate full-length PCR using the new sequence information for the design of the 5' primer.

Recombinant polypeptides of the present invention may be prepared by processes well known in the art from genetically engineered host cells comprising expression systems. Accordingly, in a further aspect, the present invention relates to expression systems comprising a polynucleotide or polynucleotides of the present invention, to host cells which are genetically engineered with such expression systems and to the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention.

For recombinant production, host cells can be genetically engineered to incorporate expression systems or portions thereof for polynucleotides of the present invention. Polynucleotides may be introduced into host cells by methods described in many standard laboratory manuals, such as Davis et al., Basic Methods in Molecular Biology (1986) and Sambrook *et al. (ibid)*. Preferred methods of introducing polynucleotides into host cells include, for instance, calcium phosphate transfection, DEAE-dextran mediated transfection, transfection, micro-injection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction or infection.

Representative examples of appropriate hosts include bacterial cells, such as *Streptococci*, *Staphylococci*, *E. coli*, *Streptomyces* and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, HEK 293 and Bowes melanoma cells; and plant cells.

A great variety of expression systems can be used, for instance, chromosomal, episomal and virus-derived systems, *e.g.*, vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression systems may contain control regions that regulate as well as engender expression. Generally, any system or vector that is able to maintain, propagate or express a polynucleotide to produce a

polypeptide in a host may be used. The appropriate polynucleotide sequence may be inserted into an expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook *et al.*, (*ibid*). Appropriate secretion signals may be incorporated into the desired polypeptide to allow secretion of the translated protein into the lumen of the endoplasmic reticulum, the periplasmic space or the extracellular environment. These signals may be endogenous to the polypeptide or they may be heterologous signals.

If a polypeptide of the present invention is to be expressed for use in screening assays, it is generally preferred that the polypeptide be produced at the surface of the cell. In this event, the cells may be harvested prior to use in the screening assay. If the polypeptide is secreted into the medium, the medium can be recovered in order to recover and purify the polypeptide. If produced intracellularly, the cells must first be lysed before the polypeptide is recovered.

Polypeptides of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during intracellular synthesis, isolation and/or purification.

Polynucleotides of the present invention may be used as diagnostic reagents, through detecting mutations in the associated gene. Detection of a mutated form of a gene is characterized by the polynucleotides set forth in the Sequence Listing in the cDNA or genomic sequence and which is associated with a dysfunction. Will provide a diagnostic tool that can add to, or define, a diagnosis of a disease, or susceptibility to a disease, which results from under-expression, over-expression or altered spatial or temporal expression of the gene. Individuals carrying mutations in the gene may be detected at the DNA level by a variety of techniques well known in the art.

Nucleic acids for diagnosis may be obtained from a subject's cells, such as from blood, urine, saliva, tissue biopsy or autopsy material. The genomic DNA may be used directly for detection or it may be amplified enzymatically by using PCR, preferably RT-PCR, or other amplification techniques prior to analysis. RNA or cDNA may also be used in similar fashion. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype. Point mutations can be identified

by hybridizing amplified DNA to labeled nucleotide sequences of the genes set forth in Table I. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence difference may also be detected by alterations in the electrophoretic mobility of DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing (see, for instance, Myers *et al.*, Science (1985) 230:1242). Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the chemical cleavage method (see Cotton *et al.*, Proc Natl Acad Sci USA (1985) 85: 4397-4401).

An array of oligonucleotide probes comprising polynucleotide sequences or fragments thereof of the genes set forth in Table I can be constructed to conduct efficient screening of *e.g.*, genetic mutations. Such arrays are preferably high density arrays or grids. Array technology methods are well known and have general applicability and can be used to address a variety of questions in molecular genetics including gene expression, genetic linkage, and genetic variability, see, for example, M. Chee *et al.*, Science, 274, 610-613 (1996) and other references cited therein.

Detection of abnormally decreased or increased levels of polypeptide or mRNA expression may also be used for diagnosing or determining susceptibility of a subject to a disease of the invention. Decreased or increased expression can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, such as, for example, nucleic acid amplification, for instance PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein, such as a polypeptide of the present invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radio-immunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

Thus in another aspect, the present invention relates to a diagnostic kit comprising:

- (a) a polynucleotide of the present invention, preferably the nucleotide sequence set forth in the Sequence Listing, or a fragment or an RNA transcript thereof;
- (b) a nucleotide sequence complementary to that of (a);
- (c) a polypeptide of the present invention, preferably the polypeptide set forth in the Sequence Listing or a fragment thereof; or
- (d) an antibody to a polypeptide of the present invention, preferably to the polypeptide set forth in the Sequence Listing.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component. Such a kit will be of use in diagnosing a disease or susceptibility to a disease, particularly diseases of the invention, amongst others.

The polynucleotide sequences of the present invention are valuable for chromosome localisation studies. The sequences set forth in the Sequence Listing are specifically targeted to, and can hybridize with, a particular location on an individual human chromosome. The mapping of relevant sequences to chromosomes according to the present invention is an important first step in correlating those sequences with gene associated disease. Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found in, for example, V. McKusick, Mendelian Inheritance in Man (available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and diseases that have been mapped to the same chromosomal region are then identified through linkage analysis (co-inheritance of physically adjacent genes). Precise human chromosomal localisations for a genomic sequence (gene fragment etc.) can be determined using Radiation Hybrid (RH) Mapping (Walter, M. Spillett, D., Thomas, P., Weissenbach, J., and Goodfellow, P., (1994) A method for constructing radiation hybrid maps of whole genomes, *Nature Genetics* 7, 22-28). A number of RH panels are available from Research Genetics (Huntsville, AL, USA) e.g. the GeneBridge4 RH panel (*Hum Mol Genet* 1996 Mar;5(3):339-46 A radiation hybrid map of the human genome. Gyapay G, Schmitt K, Fizames C, Jones H, Vega-Czarny N, Spillett D, Muselet D, Prud'Homme JF, Dib C, Auffray C, Morissette J, Weissenbach J, Goodfellow PN). To determine the chromosomal location of a gene using this panel, 93 PCRs are performed using primers designed from the gene of interest on RH DNAs. Each of these DNAs contains random human genomic fragments maintained in a hamster background (human / hamster hybrid cell lines). These PCRs result in 93 scores indicating the presence or absence of the PCR product of the gene of interest. These scores are compared with scores created using PCR products from genomic sequences of known location. This comparison is conducted at <http://www.genome.wi.mit.edu/>.

The polynucleotide sequences of the present invention are also valuable tools for tissue expression studies. Such studies allow the determination of expression patterns of polynucleotides of the present invention which may give an indication as to the expression patterns of the encoded polypeptides in tissues, by detecting the mRNAs that encode them. The techniques used are well known in the art and include in situ hybridization techniques to clones arrayed on a grid, such as cDNA microarray hybridization (Schena *et al*, *Science*, 270, 467-470, 1995 and Shalon *et al*, *Genome Res*, 6, 639-645, 1996) and nucleotide amplification techniques such as PCR. A preferred method uses the TAQMAN (Trade mark) technology available from Perkin Elmer. Results from these studies can provide an

indication of the normal function of the polypeptide in the organism. In addition, comparative studies of the normal expression pattern of mRNAs with that of mRNAs encoded by an alternative form of the same gene (for example, one having an alteration in polypeptide coding potential or a regulatory mutation) can provide valuable insights into the role of the polypeptides of the present invention, or that of inappropriate expression thereof in disease. Such inappropriate expression may be of a temporal, spatial or simply quantitative nature.

A further aspect of the present invention relates to antibodies. The polypeptides of the invention or their fragments, or cells expressing them, can be used as immunogens to produce antibodies that are immunospecific for polypeptides of the present invention. The term "immunospecific" means that the antibodies have substantially greater affinity for the polypeptides of the invention than their affinity for other related polypeptides in the prior art.

Antibodies generated against polypeptides of the present invention may be obtained by administering the polypeptides or epitope-bearing fragments, or cells to an animal, preferably a non-human animal, using routine protocols. For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler, G. and Milstein, C., *Nature* (1975) 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today* (1983) 4:72) and the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, 77-96, Alan R. Liss, Inc., 1985).

Techniques for the production of single chain antibodies, such as those described in U.S. Patent No. 4,946,778, can also be adapted to produce single chain antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms, including other mammals, may be used to express humanized antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptide or to purify the polypeptides by affinity chromatography. Antibodies against polypeptides of the present invention may also be employed to treat diseases of the invention, amongst others.

Polypeptides and polynucleotides of the present invention may also be used as vaccines. Accordingly, in a further aspect, the present invention relates to a method for inducing an immunological response in a mammal that comprises inoculating the mammal with a polypeptide of the present invention, adequate to produce antibody and/or T cell immune response, including, for example, cytokine-producing T cells or cytotoxic T cells,

to protect said animal from disease, whether that disease is already established within the individual or not. An immunological response in a mammal may also be induced by a method comprises delivering a polypeptide of the present invention *via* a vector directing expression of the polynucleotide and coding for the polypeptide *in vivo* in order to induce
5 such an immunological response to produce antibody to protect said animal from diseases of the invention. One way of administering the vector is by accelerating it into the desired cells as a coating on particles or otherwise. Such nucleic acid vector may comprise DNA, RNA, a modified nucleic acid, or a DNA/RNA hybrid. For use a vaccine, a polypeptide or a nucleic acid vector will be normally provided as a vaccine formulation (composition). The
10 formulation may further comprise a suitable carrier. Since a polypeptide may be broken down in the stomach, it is preferably administered parenterally (for instance, subcutaneous, intra-muscular, intravenous, or intra-dermal injection). Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions that may contain anti-oxidants, buffers, bacteriostats and solutes that render the formulation isotonic with the
15 blood of the recipient; and aqueous and non-aqueous sterile suspensions that may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the
20 immunogenicity of the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

Polypeptides of the present invention have one or more biological functions that are of relevance in one or more disease states, in particular the diseases of the invention
25 hereinbefore mentioned. It is therefore useful to identify compounds that stimulate or inhibit the function or level of the polypeptide. Accordingly, in a further aspect, the present invention provides for a method of screening compounds to identify those that stimulate or inhibit the function or level of the polypeptide. Such methods identify agonists or antagonists that may be employed for therapeutic and prophylactic purposes for such
30 diseases of the invention as hereinbefore mentioned. Compounds may be identified from a variety of sources, for example, cells, cell-free preparations, chemical libraries, collections of chemical compounds, and natural product mixtures. Such agonists or antagonists so-identified may be natural or modified substrates, ligands, receptors, enzymes, etc., as the case may be, of the polypeptide; a structural or functional mimetic thereof (see Coligan *et al.*, Current Protocols in Immunology 1(2):Chapter 5 (1991)) or a small molecule. Such
35

small molecules preferably have a molecular weight below 2,000 daltons, more preferably between 300 and 1,000 daltons, and most preferably between 400 and 700 daltons. It is preferred that these small molecules are organic molecules.

5 The screening method may simply measure the binding of a candidate compound to the polypeptide, or to cells or membranes bearing the polypeptide, or a fusion protein thereof, by means of a label directly or indirectly associated with the candidate compound. Alternatively, the screening method may involve measuring or detecting (qualitatively or quantitatively) the competitive binding of a candidate compound to the polypeptide against a labeled competitor (*e.g.* agonist or antagonist). Further, these screening methods may test 10 whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide, using detection systems appropriate to the cells bearing the polypeptide. Inhibitors of activation are generally assayed in the presence of a known agonist and the effect on activation by the agonist by the presence of the candidate compound is observed. Further, the screening methods may simply comprise the steps of mixing a candidate 15 compound with a solution containing a polypeptide of the present invention, to form a mixture, measuring an activity of the genes set forth in Table I in the mixture, and comparing activity of the mixture of the genes set forth in Table I to a control mixture which contains no candidate compound.

Polypeptides of the present invention may be employed in conventional low 20 capacity screening methods and also in high-throughput screening (HTS) formats. Such HTS formats include not only the well-established use of 96- and, more recently, 384-well microtiter plates but also emerging methods such as the nanowell method described by Schullek et al, *Anal Biochem.*, 246, 20-29, (1997). Fusion proteins, such as those made from Fc portion and polypeptide of the genes set forth 25 in Table I, as hereinbefore described, can also be used for high-throughput screening assays to identify antagonists for the polypeptide of the present invention (see D. Bennett *et al.*, *J Mol Recognition*, 8:52-58 (1995); and K. Johanson *et al.*, *J Biol Chem*, 270(16):9459-9471 (1995)).

The polynucleotides, polypeptides and antibodies to the polypeptide of the present 30 invention may also be used to configure screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. For example, an ELISA assay may be constructed for measuring secreted or cell associated levels of polypeptide using monoclonal and polyclonal antibodies by standard methods known in the art. This can be used to discover agents that may inhibit or enhance the production of polypeptide 35 (also called antagonist or agonist, respectively) from suitably manipulated cells or tissues.

A polypeptide of the present invention may be used to identify membrane bound or soluble receptors, if any, through standard receptor binding techniques known in the art. These include, but are not limited to, ligand binding and crosslinking assays in which the polypeptide is labeled with a radioactive isotope (for instance, ^{125}I), chemically modified
5 (for instance, biotinylated), or fused to a peptide sequence suitable for detection or purification, and incubated with a source of the putative receptor (cells, cell membranes, cell supernatants, tissue extracts, bodily fluids). Other methods include biophysical techniques such as surface plasmon resonance and spectroscopy. These screening methods may also be used to identify agonists and antagonists of the polypeptide that compete with the binding of
10 the polypeptide to its receptors, if any. Standard methods for conducting such assays are well understood in the art.

Examples of antagonists of polypeptides of the present invention include antibodies or, in some cases, oligonucleotides or proteins that are closely related to the ligands, substrates, receptors, enzymes, etc., as the case may be, of the polypeptide, *e.g.*, a fragment
15 of the ligands, substrates, receptors, enzymes, etc.; or a small molecule that bind to the polypeptide of the present invention but do not elicit a response, so that the activity of the polypeptide is prevented.

Screening methods may also involve the use of transgenic technology and the genes set forth in Table I. The art of constructing transgenic animals is well established. For
20 example, the genes set forth in Table I may be introduced through microinjection into the male pronucleus of fertilized oocytes, retroviral transfer into pre- or post-implantation embryos, or injection of genetically modified, such as by electroporation, embryonic stem cells into host blastocysts. Particularly useful transgenic animals are so-called "knock-in" animals in which an animal gene is replaced by the human equivalent within the genome of
25 that animal. Knock-in transgenic animals are useful in the drug discovery process, for target validation, where the compound is specific for the human target. Other useful transgenic animals are so-called "knock-out" animals in which the expression of the animal ortholog of a polypeptide of the present invention and encoded by an endogenous DNA sequence in a cell is partially or completely annulled. The gene knock-out may be targeted to specific
30 cells or tissues, may occur only in certain cells or tissues as a consequence of the limitations of the technology, or may occur in all, or substantially all, cells in the animal. Transgenic animal technology also offers a whole animal expression-cloning system in which introduced genes are expressed to give large amounts of polypeptides of the present invention

Screening kits for use in the above described methods form a further aspect of the present invention. Such screening kits comprise:

- (a) a polypeptide of the present invention;
 - (b) a recombinant cell expressing a polypeptide of the present invention;
 - 5 (c) a cell membrane expressing a polypeptide of the present invention; or
 - (d) an antibody to a polypeptide of the present invention;
- which polypeptide is preferably that set forth in the Sequence Listing.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component.

10

Glossary

The following definitions are provided to facilitate understanding of certain terms used frequently hereinbefore.

- “Antibodies” as used herein includes polyclonal and monoclonal antibodies, chimeric,
 15 single chain, and humanized antibodies, as well as Fab fragments, including the products of an
 Fab or other immunoglobulin expression library.

- “Isolated” means altered “by the hand of man” from its natural state, *i.e.*, if it occurs in nature, it has been changed or removed from its original environment, or both. For
 20 example, a polynucleotide or a polypeptide naturally present in a living organism is not “isolated,” but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is “isolated”, as the term is employed herein. Moreover, a polynucleotide or polypeptide that is introduced into an organism by transformation, genetic manipulation or by any other recombinant method is “isolated” even if it is still present in
 25 said organism, which organism may be living or non-living.

- “Secreted protein activity or secreted polypeptide activity” or “biological activity of the secreted protein or secreted polypeptide” refers to the metabolic or physiologic function of said secreted protein including similar activities or improved activities or these activities with decreased undesirable side-effects. Also included are antigenic and immunogenic
 30 activities of said secreted protein.

“Secreted protein gene” refers to a polynucleotide comprising any of the attached nucleotide sequences or allelic variants thereof and/or their complements.

“Polynucleotide” generally refers to any polyribonucleotide (RNA) or polydeoxiribonucleotide (DNA), which may be unmodified or modified RNA or DNA.

- 35 “Polynucleotides” include, without limitation, single- and double-stranded DNA, DNA that

is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, "polynucleotide" refers to triple-
5 stranded regions comprising RNA or DNA or both RNA and DNA. The term "polynucleotide" also includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications may be made to DNA and RNA; thus, "polynucleotide" embraces chemically,
10 enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. "Polynucleotide" also embraces relatively short polynucleotides, often referred to as oligonucleotides.

"Polypeptide" refers to any polypeptide comprising two or more amino acids joined
15 to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. "Polypeptide" refers to both short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. "Polypeptides" include amino acid sequences modified either by natural processes, such as post-translational
20 processing, or by chemical modification techniques that are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications may occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present to the
25 same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from post-translation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-
30 ribosylation, amidation, biotinylation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation,
35 glycosylation, GPI anchor formation, hydroxylation, iodination, methylation,

myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination (see, for instance, *Proteins - Structure and Molecular Properties*, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993; Wold, F., *Post-translational Protein Modifications: Perspectives and Prospects*, 1-12, in *Post-translational Covalent Modification of Proteins*, B. C. Johnson, Ed., Academic Press, New York, 1983; Seifter *et al.*, "Analysis for protein modifications and nonprotein cofactors", *Meth Enzymol*, 182, 626-646, 1990, and Rattan *et al.*, "Protein Synthesis: Post-translational Modifications and Aging", *Ann NY Acad Sci*, 663, 48-62, 1992).

10 "Fragment" of a polypeptide sequence refers to a polypeptide sequence that is shorter than the reference sequence but that retains essentially the same biological function or activity as the reference polypeptide. "Fragment" of a polynucleotide sequence refers to a polynucleotide sequence that is shorter than the reference sequence set forth in the Sequence Listing.

15 "Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains the essential properties thereof. A typical variant of a polynucleotide differs in nucleotide sequence from the reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes
20 may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from the reference polypeptide. Generally, alterations are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide
25 may differ in amino acid sequence by one or more substitutions, insertions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. Typical conservative substitutions include Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe and Tyr. A variant of a polynucleotide or polypeptide may be naturally occurring such as an allele, or it may be a variant that is not
30 known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis. Also included as variants are polypeptides having one or more post-translational modifications, for instance glycosylation, phosphorylation, methylation, ADP ribosylation and the like. Embodiments include methylation of the N-terminal amino acid, phosphorylations of
35 serines and threonines and modification of C-terminal glycines.

"Allele" refers to one of two or more alternative forms of a gene occurring at a given locus in the genome.

"Polymorphism" refers to a variation in nucleotide sequence (and encoded polypeptide sequence, if relevant) at a given position in the genome within a population.

5 "Single Nucleotide Polymorphism" (SNP) refers to the occurrence of nucleotide variability at a single nucleotide position in the genome, within a population. An SNP may occur within a gene or within intergenic regions of the genome. SNPs can be assayed using Allele Specific Amplification (ASA). For the process at least 3 primers are required. A common primer is used in reverse complement to the polymorphism being assayed. This
10 common primer can be between 50 and 1500 bps from the polymorphic base. The other two (or more) primers are identical to each other except that the final 3' base wobbles to match one of the two (or more) alleles that make up the polymorphism. Two (or more) PCR reactions are then conducted on sample DNA, each using the common primer and one of the Allele Specific Primers.

15 "Splice Variant" as used herein refers to cDNA molecules produced from RNA molecules initially transcribed from the same genomic DNA sequence but which have undergone alternative RNA splicing. Alternative RNA splicing occurs when a primary RNA transcript undergoes splicing, generally for the removal of introns, which results in the production of more than one mRNA molecule each of that may encode different amino acid
20 sequences. The term splice variant also refers to the proteins encoded by the above cDNA molecules.

"Identity" reflects a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, determined by comparing the sequences. In general, identity refers to an exact nucleotide to nucleotide or amino acid to amino acid
25 correspondence of the two polynucleotide or two polypeptide sequences, respectively, over the length of the sequences being compared.

"% Identity" - For sequences where there is not an exact correspondence, a "% identity" may be determined. In general, the two sequences to be compared are aligned to give a maximum correlation between the sequences. This may include inserting "gaps" in
30 either one or both sequences, to enhance the degree of alignment. A % identity may be determined over the whole length of each of the sequences being compared (so-called global alignment), that is particularly suitable for sequences of the same or very similar length, or over shorter, defined lengths (so-called local alignment), that is more suitable for sequences of unequal length.

"Similarity" is a further, more sophisticated measure of the relationship between two polypeptide sequences. In general, "similarity" means a comparison between the amino acids of two polypeptide chains, on a residue by residue basis, taking into account not only exact correspondences between a between pairs of residues, one from each of the sequences
5 being compared (as for identity) but also, where there is not an exact correspondence, whether, on an evolutionary basis, one residue is a likely substitute for the other. This likelihood has an associated "score" from which the "% similarity" of the two sequences can then be determined.

Methods for comparing the identity and similarity of two or more sequences are well known in the art. Thus for instance, programs available in the Wisconsin Sequence
10 Analysis Package, version 9.1 (Devereux J et al, Nucleic Acids Res, 12, 387-395, 1984, available from Genetics Computer Group, Madison, Wisconsin, USA), for example the programs BESTFIT and GAP, may be used to determine the % identity between two polynucleotides and the % identity and the % similarity between two polypeptide sequences.
15 BESTFIT uses the "local homology" algorithm of Smith and Waterman (J Mol Biol, 147,195-197, 1981, Advances in Applied Mathematics, 2, 482-489, 1981) and finds the best single region of similarity between two sequences. BESTFIT is more suited to comparing two polynucleotide or two polypeptide sequences that are dissimilar in length, the program assuming that the shorter sequence represents a portion of the longer. In comparison, GAP
20 aligns two sequences, finding a "maximum similarity", according to the algorithm of Needleman and Wunsch (J Mol Biol, 48, 443-453, 1970). GAP is more suited to comparing sequences that are approximately the same length and an alignment is expected over the entire length. Preferably, the parameters "Gap Weight" and "Length Weight" used in each program are 50 and 3, for polynucleotide sequences and 12 and 4 for polypeptide sequences,
25 respectively. Preferably, % identities and similarities are determined when the two sequences being compared are optimally aligned.

Other programs for determining identity and/or similarity between sequences are also known in the art, for instance the BLAST family of programs (Altschul S F et al, J Mol Biol, 215, 403-410, 1990, Altschul S F et al, Nucleic Acids Res., 25:389-3402, 1997,
30 available from the National Center for Biotechnology Information (NCBI), Bethesda, Maryland, USA and accessible through the home page of the NCBI at www.ncbi.nlm.nih.gov) and FASTA (Pearson W R, Methods in Enzymology, 183, 63-99, 1990; Pearson W R and Lipman D J, Proc Nat Acad Sci USA, 85, 2444-2448,1988, available as part of the Wisconsin Sequence Analysis Package).

Preferably, the BLOSUM62 amino acid substitution matrix (Henikoff S and Henikoff J G, Proc. Nat. Acad Sci. USA, 89, 10915-10919, 1992) is used in polypeptide sequence comparisons including where nucleotide sequences are first translated into amino acid sequences before comparison.

- 5 Preferably, the program BESTFIT is used to determine the % identity of a query polynucleotide or a polypeptide sequence with respect to a reference polynucleotide or a polypeptide sequence, the query and the reference sequence being optimally aligned and the parameters of the program set at the default value, as hereinbefore described.

- 10 "Identity Index" is a measure of sequence relatedness which may be used to compare a candidate sequence (polynucleotide or polypeptide) and a reference sequence. Thus, for instance, a candidate polynucleotide sequence having, for example, an Identity Index of 0.95 compared to a reference polynucleotide sequence is identical to the reference sequence except that the candidate polynucleotide sequence may include on average up to five differences per each 100 nucleotides of the reference sequence. Such differences are
15 selected from the group consisting of at least one nucleotide deletion, substitution, including transition and transversion, or insertion. These differences may occur at the 5' or 3' terminal positions of the reference polynucleotide sequence or anywhere between these terminal positions, interspersed either individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. In other words, to
20 obtain a polynucleotide sequence having an Identity Index of 0.95 compared to a reference polynucleotide sequence, an average of up to 5 in every 100 of the nucleotides of the in the reference sequence may be deleted, substituted or inserted, or any combination thereof, as hereinbefore described. The same applies *mutatis mutandis* for other values of the Identity Index, for instance 0.96, 0.97, 0.98 and 0.99.

- 25 Similarly, for a polypeptide, a candidate polypeptide sequence having, for example, an Identity Index of 0.95 compared to a reference polypeptide sequence is identical to the reference sequence except that the polypeptide sequence may include an average of up to five differences per each 100 amino acids of the reference sequence. Such differences are selected from the group consisting of at least one amino acid deletion, substitution,
30 including conservative and non-conservative substitution, or insertion. These differences may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between these terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. In other words, to obtain a polypeptide sequence having an
35 Identity Index of 0.95 compared to a reference polypeptide sequence, an average of up to 5

in every 100 of the amino acids in the reference sequence may be deleted, substituted or inserted, or any combination thereof, as hereinbefore described. The same applies *mutatis mutandis* for other values of the Identity Index, for instance 0.96, 0.97, 0.98 and 0.99.

5 The relationship between the number of nucleotide or amino acid differences and the Identity Index may be expressed in the following equation:

$$n_a \leq x_a - (x_a \cdot I),$$

in which:

n_a is the number of nucleotide or amino acid differences,

10 x_a is the total number of nucleotides or amino acids in a sequence set forth in the Sequence Listing,

I is the Identity Index,

\cdot is the symbol for the multiplication operator, and

in which any non-integer product of x_a and I is rounded down to the nearest integer prior to subtracting it from x_a .

15 "Homolog" is a generic term used in the art to indicate a polynucleotide or polypeptide sequence possessing a high degree of sequence relatedness to a reference sequence. Such relatedness may be quantified by determining the degree of identity and/or similarity between the two sequences as hereinbefore defined. Falling within this generic term are the terms "ortholog", and "paralog". "Ortholog" refers to a polynucleotide or
20 polypeptide that is the functional equivalent of the polynucleotide or polypeptide in another species. "Paralog" refers to a polynucleotide or polypeptide that within the same species which is functionally similar.

"Fusion protein" refers to a protein encoded by two, often unrelated, fused genes or fragments thereof. In one example, EP-A-0 464 533-A discloses fusion proteins comprising
25 various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, employing an immunoglobulin Fc region as a part of a fusion protein is advantageous for use in therapy and diagnosis resulting in, for example, improved pharmacokinetic properties [see, *e.g.*, EP-A 0232 262]. On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion
30 protein has been expressed, detected and purified.

All publications and references, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference in their entirety as if each individual publication or reference were specifically and individually indicated to be incorporated by reference herein as being fully set forth. Any patent application to which

this application claims priority is also incorporated by reference herein in its entirety in the manner described above for publications and references.

Table I.

Gene Name	GSK Gene ID	Nucleic Acid SEQ ID NO's	Corresponding Protein SEQ ID NO's
sbg960509cbrept	960509	SEQ ID NO:1	SEQ ID NO:45
sbg614126complfh	614126	SEQ ID NO:2	SEQ ID NO:46
		SEQ ID NO:3	SEQ ID NO:47
sbg120703RNase	120703	SEQ ID NO:4	SEQ ID NO:48
sbg98530TS	98530	SEQ ID NO:5	SEQ ID NO:49
		SEQ ID NO:6	SEQ ID NO:50
sbg563917RDP	63917	SEQ ID NO:7	SEQ ID NO:51
		SEQ ID NO:8	SEQ ID NO:52
sbg618069LRR	618069	SEQ ID NO:9	SEQ ID NO:53
		SEQ ID NO:10	SEQ ID NO:54
sbg934114Relaxin	934114	SEQ ID NO:11	SEQ ID NO:55
sbg99174LOX-like	99174	SEQ ID NO:12	SEQ ID NO:56
sbg995002PIGR	995002	SEQ ID NO:13	SEQ ID NO:57
sbg1033026C1q	1033026	SEQ ID NO:14	SEQ ID NO:58
		SEQ ID NO:15	SEQ ID NO:59
sbg1003675RNase	1003675	SEQ ID NO:16	SEQ ID NO:60
sbg1015258PLM	1015258	SEQ ID NO:17	SEQ ID NO:61
sbg1003328IG	1003328	SEQ ID NO:18	SEQ ID NO:62
		SEQ ID NO:19	SEQ ID NO:63
sbg1020829SGLT	1020829	SEQ ID NO:20	SEQ ID NO:64
sbg1005450UDPGT	1005450	SEQ ID NO:21	SEQ ID NO:65
		SEQ ID NO:22	SEQ ID NO:66
sbg1002620TIa	1002620	SEQ ID NO:23	SEQ ID NO:67
		SEQ ID NO:24	SEQ ID NO:68
sbg1002620TIb	1002620	SEQ ID NO:25	SEQ ID NO:69
sbg102200MCTa	102200	SEQ ID NO:26	SEQ ID NO:70
		SEQ ID NO:27	SEQ ID NO:71
sbg102200MCTb	102200	SEQ ID NO:28	SEQ ID NO:72
sbg1020380LYG	1020380	SEQ ID NO:29	SEQ ID NO:73
		SEQ ID NO:30	SEQ ID NO:74
sbg1007026SGLT	1007026	SEQ ID NO:31	SEQ ID NO:75
sbg1012732GLUT	1012732	SEQ ID NO:32	SEQ ID NO:76
		SEQ ID NO:33	SEQ ID NO:77
sbg1012732GLUTb	1012732	SEQ ID NO:34	SEQ ID NO:78
sbg1018172CSP	1018172	SEQ ID NO:35	SEQ ID NO:79
		SEQ ID NO:36	SEQ ID NO:80
sbg1004570ERGIC	1004570	SEQ ID NO:37	SEQ ID NO:81
		SEQ ID NO:38	SEQ ID NO:82
sbg1016995IGBrecpt	1016995	SEQ ID NO:39	SEQ ID NO:83
		SEQ ID NO:40	SEQ ID NO:84
sbg1151bSREC	1151	SEQ ID NO:41	SEQ ID NO:85
		SEQ ID NO:42	SEQ ID NO:86
sbg1399854ANK	1399854	SEQ ID NO:43	SEQ ID NO:87
		SEQ ID NO:44	SEQ ID NO:88

Table II

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg960509 cbrectp	Carbohydrate-binding receptor	GB:AC007395 Direct submitted (25-APR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	Mouse Kupffer cell c-type lectin receptor, gi: 7949066 Submitted (25-OCT-1996) to the DDBJ/EMBL/GenBank databases.	Membrane-bound
sbg614126 complfH	Complement factor H	SC:AL353809 Submitted (20-JAN-2001) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Human H-factor like 1, gi:11321587 Estaller,C., Koistinen,V., Schwaeble,W., Dierich,M.P., and Weiss,E.H. J. Immunol. 146, 3190-3196 (1991)	Secreted
sbg120703 RNase	RNase	GB:AL157687 Direct Submitted (24-MAY-2000) to the EMBL/GenBank/DDBJ databases by Genoscope.	Human keratinocyte-derived RNase-like protein, geneseq: Y44192 Submitted by INNOGENETICS NV Application number and publication date: EP-943679-A1, 22-SEP-99	Secreted
sbg98530T S	Thrombospondin type I	GB:AC027307 Submitted (30-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	Mouse RIKEN cDNA 2010109H09 gene, gi:13385092 The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium. Nature 409, 685-690 (2001)	Secreted
sbg563917 RDP	Renal dipeptidase	GB:AC009077 Directly submitted (03-AUG-1999) by Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	Human putative metallopeptidase (family M19) gi:11641273 Chen,J.M., Fortunato,M. and Barrett, A.J. Submitted (02-NOV-2000) Chen J.M., MRC Molecular Enzymology Laboratory, The Babraham Institute, Babraham, Cambridge, CB2 4AT, UK	Secreted

Table II (cont).

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg618069 LRR	Leucine-rich repeat	GB:AL589765 Submitted (16-MAR-2001) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Macaca fascicularis brain protein, gi: 9651088 Submitted (28-JUL-2000) to the DDBJ/EMBL/GenBank databases. Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan	Membrane-bound
sbg934114 Relaxin	Insulin	JGI:CIT978SKB_5506 Found at Joint Genome Institute DoE/LLNL/LBNL/LANL.	Mouse insulin-like peptide (relaxin/insulin-like protein), gi:7387805 Conklin D, Lofton-Day CE, Haldeman BA, Ching A, Whitmore TE, Lok S, Jaspers S. 1999. Genomics 60:50-56.	Secreted
sbg99174L OX-like	C-type lectin	GB:AL137062 Direct submitted (09-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Mouse putative protien, gi: 12855891 The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium. Nature 409, 685-690 (2001)	Membrane-bound
sbg995002 PIGR	Polymeric - immublob ulin receptor (PIGR)	GB:AC027192 Direct submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.	Human TANGO 354 protein, geneseqp: B66271 Submitted by (MILL-) MILLENNIUM PHARM INC Application number and publication date: WO200100673-A1, 04-JAN-01	Membrane-bound
sbg103302 6Clq	Clq	GB:AL359736 Direct submitted (22-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Human adipocyte-specific secretory protein, gi: 4757760 Maeda,K., Okubo,K., Shimomura,I., Funahashi,T., Matsuzawa,Y. and Matsubara,K. Biochem. Biophys. Res. Commun. 221 (2), 286-289 (1996)	Secreted

Table II (cont).

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg100367 5RNase	RNase	EMBL:CNS01RIH Found at European Molecular Biology Laboratory.	Chinchilla brevicaudata pancreatic ribonuclease, gi:133205 Van Den Berg A, Van Den Hende-Timmer L, Beintema JJ. 1976. Biochim Biophys Acta 453:400-9.	Secreted
sbg101525 8PLM	Phospholemman (PLM)	GB:AL022345 Direct submitted (10-DEC-1999) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Human phospholemman-like protein, geneseq:W51104 Submitted by (HUMA-) HUMAN GENOME SCI INC Application number and publication date: WO9839448-A2, 11-SEP-98	Membrane-bound
sbg100332 8IG	Immunoglobulin	EMBL:HSBA536C5 Found at European Molecular Biology Laboratory.	Human immune system molecule, geneseq:B15536 Submitted by (INCY-) INCYTE PHARM INC Application number and publication date: WO200060080-A2, 12-OCT-00	Membrane-bound
sbg102082 9SGLT	Na ⁺ /glucose cotransporter	GB:AJ009617 Directly submitted (17-JUL-1998) by MPIMG, Abt.Lehrach, Max Planck Institut fuer Molekulare Genetik, Ihnestrass 73, Berlin, 14195, Germany.	Oryctolagus cuniculus Na ⁺ /glucose cotransporters, gi:520469 Pajor,A.M. 1994 Biochim. Biophys. Acta 1194 (2), 349-51.	Membrane-bound
sbg100545 0UDPGT	UDP-glucuronosyltransferase(UDPGT)	GB:AC016612 Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	Human PRO1780 protein , geneseq: B24025 Submitted by GENENTECH INC Application number and publication date: WO200053750-A1, 14-SEP-00	Membrane-bound
sbg100262 0TIa	Cysteine-rich secretory protein (CRISP) trypsin inhibitor	GB:AC025280 Submitted (08-MAR-2000) by Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	Human hypothetical protein DKFZp434B044, gi: 13899332 Wiemann,S., Weil,B. et al. Genome Res. 11 (3), 422-435 (2001)	Secreted

Table II (cont).

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg100262 OTIb	Cysteine-rich secretory protein (CRISP) trypsin inhibitor	GB:AC025280 Submitted (08-MAR-2000) by Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	Rat late gestation lung protein 1, gi:4324682 Kaplan, F., Ledoux, P., Kassamali, F.Q., Gagnon, S., Post, M., Koehler, D., Deimling, J. and Swezey, N.B. Am. J. Physiol. 276 (6), L1027-L1036 (1999)	Secreted
sbg102200 MCTa	Monocarboxylate cotransporter (MCT1)	GB: AC015918 Directly submitted (17-NOV-1999) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.	Mouse unnamed protein product, gi:7670446 Submitted (12-APR-2000) to the DDBJ/EMBL/GenBank databases by Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan	Membrane-bound
sbg102200 MCTb	Monocarboxylate cotransporter (MCT1)	GB: AC015918 Directly submitted (17-NOV-1999) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.	Human solute carrier 16 (monocarboxylic acid transporters), member 8, gi:13655082 Submitted (17-APR-2001) by National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA	Membrane-bound
sbg102038 OLYG	Goose-type lysozyme G	GB:AC023965 Directly submitted (20-FEB-2000) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	Lysozyme G (1,4-beta-N-acetylmuramidase) (Goose-type lysozyme). gi:126634 Schoentgen, F., Jolles, J. and Jolles, P. Eur. J. Biochem. 123 (3), 489-497 (1982)	Secreted
sbg100702 6SGLT	Sodium-glucose cotransporter	GB:AC046167 Direct submitted (13-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141.	Human transport protein TPPT-13, gene seq: B60093 Submitted by INCYTE GENOMICS INC Application number and publication date: WO200078953-A2, 28-DEC-00	Membrane-bound

Table II (cont).

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg101273 2GLUT	Glucose transporter	GB:AP000350 Direct submitted (10-JUN-1999) to the DDBJ/EMBL/GenBank databases. Nobuyoshi Shimizu, Keio university, school of medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-0016, Japan.	Human glucose transporter GLUT10, gi:13540598 Submitted (10-FEB-2000) Joost H.G., Institute of Pharmacology and Toxicology, Medical Faculty, Technical University of Aachen, Wendlingweg 2, Aachen, D-52057, GERMANY	Membrane-bound
sbg101273 2GLUTb	Glucose transporter	GB:AP000350 Direct submitted (10-JUN-1999) to the DDBJ/EMBL/GenBank databases. Nobuyoshi Shimizu, Keio university, school of medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-0016, Japan.	Human glucose transporter GLUT10, gi:13540598 Submitted (10-FEB-2000) Joost H.G., Institute of Pharmacology and Toxicology, Medical Faculty, Technical University of Aachen, Wendlingweg 2, Aachen, D-52057, GERMANY	Membrane-bound
sbg101817 2CSP	Chondroitin sulfate proteoglycan	EMBL:AL354819, and SC:AL590007. Submitted (30-APR-2001 and 04-MAY-2001) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. EMBL:AC017111, Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	Lytechinus variegatus embryonic blastocoelar extracellular matrix protein, gi:9837426 Submitted (14-JUL-2000) Biological Sciences, Carnegie Mellon University, 4400 Fifth Ave, Pittsburgh, PA 15213, USA	Secreted
sbg100457 OERGIC	ER-Golgi intermediate compartment protein	GB:AC020705 Submitted (08-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	Human ERGL protein, gi:11141891 Submitted (06-SEP-2000) Laboratory of Molecular Biology, NCI, NIH, 37 Convent Dr., Bldg. 37, Rm. 4B20, Bethesda, MD 20892, USA	Membrane-bound

Table II (cont).

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg101699 5IGBrecpt	Immunogl obulin receptor	GB:AL353721 Submitted (07-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Human immunoglobulin superfamily receptor translocation associated 1, gi:14550416 Hatzivassiliou,G., Miller,I.J., Takizawa,J., et al. Immunity 14 (3), 277-289 (2001)	Membrane- bound
sbg1151bS REC	EGF-like LDL receptor protein	GB:AC005500 Chen,F., D,L., Do,T., Dumanski,J.P. and Roe,B.A. Direct submission (31-MAY-01) Department Of Chemistry and Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	Human nurse cell receptor B6TNC#10b, geneseq: B60395 Submitted by (SHIO) SHIONOGI & CO LTD Application number and publication date: JP2000308492-A, 07-NOV-00	Membrane- bound
sbg139985 4ANK	The ankyrin repeat family	GB: AC020658 Direct submitted (08- JAN-2000) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA	Human KIAA1223 protein, gi:6330617 Nagase T, Ishikawa K, Kikuno R, Hirosawa M, Nomura N, and Ohara O; 1999 DNA Res 6:337-45.	Cytosolic

Table III

Gene Name	Uses	Associated Diseases
sbg960509 cbrept	<p>An embodiment of the invention is the use of sbg960509cbrept in the treatment or diagnosis of cancer. A close homologue of sbg960509cbrept is Langerin. Langerin was a type II Ca²⁺-dependent lectin, an endocytic receptor and expressed by Langerhans cells (LC). Transfection of Langerin cDNA into fibroblasts created a compact network of membrane structures with typical features of Birbeck granules(BG). It was proposed that induction of BG was a consequence of the antigen-capture function of Langerin, allowing routing into these organelles and providing access to a nonclassical antigen-processing pathway (Valladeau J, Ravel O, Dezutter-Dambuyant C, Moore K, Kleijmeer M, Liu Y, Duvert-Frances V, Vincent C, Schmitt D, Davoust J, Caux C, Lebecque S, Saeland S. 2000. <i>Immunity</i> Jan;12(1):71-81). A striking incongruity was found between variably spliced transcripts for the second asialoglycoprotein receptor polypeptide, H2, in normal and transformed human liver cells (Paietta E, Stockert RJ, Racevskis J. 1992. <i>Hepatology</i> Mar;15(3):395-402). Human macrophage cell surface C-type lectin was demonstrated to recognize Tn Ag, a well-known human carcinoma-associated epitope (Suzuki N, Yamamoto K, Toyoshima S, Osawa T, Irimura T. 1996. <i>J Immunol</i> Jan 1;156(1):128-35).</p>	Autoimmune disorder and cancer
sbg614126 complfH	<p>An embodiment of the invention is the use of sbg614126complfH in the diagnosis or treatment of cancer, Alzheimer disease, and/or tumor cell evasion. A close homologue of sbg614126complfH is Human complement factor H. Human complement factor H was detected by the AM34 antibody in the cerebrospinal fluid from an Alzheimer's disease patient. It was recently found that AM34 was capable of staining senile plaques positively and factor H was associated with senile plaques in the human brain (Honda S, Itoh F, Yoshimoto M, Ohno S, Hinoda Y, Imai K. 2000. <i>J Gerontol A Biol Sci Med Sci</i>. May;55(5):M265-9). It was also suggested that exceptional resistance of human H2 glioblastoma cells to complement-mediated killing was due to the production and binding of factor H and factor H-like protein 1 (Junnikkala S, Jokiranta TS, Friese MA, Jarva H, Zipfel PF, Meri S. 2000. <i>J Immunol</i>. Jun 1;164(11):6075-81). Moreover, factor H was shown to bind to bone sialoprotein and osteopontin and enable tumor cell evasion of complement-mediated attack (Fedarko NS, Fohr B, Robey PG, Young MF, Fisher LW. 2000. <i>J Biol Chem</i>. Jun 2;275(22):16666-72). Finally, complement factor H gene mutation was associated with autosomal recessive atypical hemolytic uremic syndrome (Ying L, Katz Y, Schlesinger M, Carmi R, Shalev H, Haider N, Beck G, Sheffield VC, Landau D. 1999. <i>Am J Hum Genet</i> Dec;65(6):1538-46).</p>	Alzheimer's disease, cancer, tumor metastasis and autosomal recessive atypical hemolytic uremic syndrome

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg120703 RNase	An embodiment of the invention is the use of sbg120703RNase as a tool for anticancer therapy, and treating apoptosis-related disorders. It has been shown that a genetic-engineered pancreatic RNase has cytotoxic action on mouse and human tumor cells, but lacks any appreciable toxicity on human and mouse normal cells. This variant of human pancreatic RNase selectively sensitized cells derived from a human thyroid tumor to apoptotic death. Because of its selectivity for tumor cells, and because of its human origin, this protein is thought to represent a promising tool for anticancer therapy (Piccoli R, Di Gaetano S, De Lorenzo C, Grauso M, Monaco C, Spalletti-Cernia D, Laccetti P, Cinatl J, Matousek J, D'Alessio G. 1999. Proc Natl Acad Sci U S A 96:7768-73). In addition, RNase itself can be used to treat an RNA viral infection, and its antagonist may be useful in treating apoptosis-related disorders.	Cancer and infection
sbg98530TS	An embodiment of the invention is the use of sbg98530TS in the wound healing processes, development of the nervous system, and affecting cell migration, survival, or angiogenesis. Close homologues of sbg98530TS are thrombospondins. The thrombospondins are a family of proteins found widely in the embryonic extracellular matrix, and the expression patterns and in vitro properties of many thrombospondins suggest potential roles in the guidance of cell and growth cone migration, especially during the development of the nervous system (Adams JC, 2000. Tucker RP Dev Dyn 218:280-99). Cell interactions with extracellular matrices are important to pathological changes that occur during cell transformation and tumorigenesis. The thrombospondin-1 has been suggested to modulate tumor phenotype by affecting cell migration, survival, or angiogenesis (Liaw L, Crawford HC. 1999. Braz J Med Biol Res 32:805-12). In addition, thrombospondin-1 is also a transient component of extracellular matrix in developing and repairing tissues (Adams JC. 1997. Int J Biochem Cell Biol 29:861-5).	Cancer, wound healing disorders
sbg563917 RDP	An embodiment of the invention is the use of sbg563917RDP in treatment or diagnosis of chronic renal failure and aged eye lenses and cataracts. Close homologues of sbg563917RDP are renal and lens dipeptidases. It has been reported that the renal dipeptidase activity was significantly lower in the chronic renal failure group (Fukumura Y, Kera Y, Oshitani S, Ushijima Y, Kobayashi I, Liu Z, Watanabe T, Yamada R, Kikuchi H, Kawazu S and Yabuuchi M. 1999 Ann Clin Biochem Mar;36 (Pt 2):221-5). In contrast, increased lens dipeptidase activity was detected in aging and cataracts (Sulochana KN, Ramakrishnan S and Punitham R. 1999 Br J Ophthalmol Jul;83(7):885).	Renal diseases, aging, cataract, cancer, and Alzheimer disease

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg618069 LRR	An embodiment of the invention is the use of sbg618069LRR in treatment or diagnosis of neural development and the adult nervous system disorders. Close homologues of sbg618069LRR are Leucine-rich repeat proteins. Leucine-rich repeat protein, the spineless-aristapedia, has been shown to interact with tango bHLH-PAS proteins for controlling antennal and tarsal development in <i>Drosophila</i> (Emmons RB, Duncan D, Estes PA, Kiefel P, Mosher JT, Sonnenfeld M, Ward MP, Duncan I and Crews ST. 1999. <i>Development</i> Sep;126(17):3937-45). In mouse, neuronal Leucine-Rich Repeat NLRR-1 and NLRR-2 mRNAs were expressed primarily in the central nervous system and may play significant but distinct roles in neural development and in the adult nervous system (Taguchi A, Wanaka A, Mori T, Matsumoto K, Imai Y, Tagaki T and Tohyama M. 1996. <i>Brain Res Mol Brain Res</i> Jan;35(1-2):31-40). Furthermore, a new member of the leucine-rich repeat superfamily GAC1 was amplified and overexpressed in malignant gliomas (Almeida A, Zhu XX, Vogt N, Tyagi R, Muleris M, Dutrillaux AM, Dutrillaux B, Ross D, Malfoy B and Hanash S. 1998. <i>Oncogene</i> Jun 11;16(23):2997-3002).	Tango-associated diseases, disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, cancer, wound healing and tissue repair
sbg934114 Relaxin	An embodiment of the invention is the use of sbg934114Relaxin in treatment or diagnosis of collagen remodeling, breast cancer, and uterine contractile disorders. A close homologue of sbg934114Relaxin is Relaxin. Relaxin has various biologic activities, including the induction of collagen remodeling and consequent softening of the tissues of the birth canal during delivery, the inhibition of uterine contractile activity, and the stimulation of growth and differentiation of the mammary gland (Bani D. 1997. <i>Gen Pharmacol</i> 28:13-22). Relaxin belongs to the insulin superfamily, and is produced primarily by the corpus luteum in both pregnant and nonpregnant females. In males, relaxin is synthesized in the prostate and released in the seminal fluid (Goldsmith LT, Weiss G, Steinetz BG. 1995. <i>Endocrinol Metab Clin North Am</i> 24:171-86). It has been further demonstrated that relaxin regulates growth and differentiation of breast cancer cells in culture, promotes dilation of blood vessels in several organs, including the uterus, the mammary gland, the lung and the heart, has a chronotropic action on the heart, inhibits the release of histamine by mast cells, depresses aggregation of platelets and their release by megakaryocytes, and influences the secretion of hormones by the pituitary gland (Bani D. 1997. <i>Gen Pharmacol</i> 28:13-22). In addition, some reports have shown that relaxin is effective in decreasing skin involvement in systemic sclerosis (Furst DE. 1998. <i>Curr Opin Rheumatol</i> 10:123-8).	Cancer, rheumatic diseases, heart diseases, systemic sclerosis (scleroderma), and preterm birth

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg99174L OX-like	An embodiment of the invention is the use of sbg99174LOX-like in treatment or diagnosis of endothelial function or atherosclerosis. A close homologue of sbg99174LOX-like is oxidized low-density lipoprotein receptor 1. sbg99174LOX-like as well as oxidized low-density lipoprotein receptor 1, contain a C-type lectin domain (CTL) (Colonna M, Samaridis J, Angman L. 2000. Eur J Immunol 30:697-704). Evidence suggests that oxidized low-density lipoprotein (OxLDL) plays a critical role in the changes in endothelial function. Lectin-like OxLDL receptor-1 (LOX-1) is the major endothelial OxLDL receptor. Functional changes of endothelial cells are implicated in the earliest stage of the pathogenesis of atherosclerosis (Aoyama T, Sawamura T, Furutani Y, Matsuoka R, Yoshida MC, Fujiwara H, Masaki T. Biochem J. 1999 339 (Pt 1):177-84).	Cardiovascular disorders (e.g. atherosclerosis, hypertension, stroke),
sbg995002 PIGR	An embodiment of the invention is the use of sbg995002PIGR to actively transport IgA and IgM to the apical surface of epithelia. A close homologue of sbg995002PIGR is polymeric-immunoglobulin receptor. The polymeric-immunoglobulin receptor binds polymeric IgA and IgM at the basolateral surface of epithelial cells. PIGR knockout mice completely lack active external IgA and IgM translocation, but remain normal and fertile (Johansen FE, Pekna M, Norderhaug IN, Haneberg B, Hietala MA, Krajci P, Betsholtz C, Brandtzaeg P. 1999. J Exp Med 190:915-22). In addition, it has been reported that PIGR can be upregulated by tumor necrosis factor (TNF)-alpha (Takenouchi-Ohkubo N, Takahashi T, Tsuchiya M, Mestecky J, Moldoveanu Z, Moro I; 2000. Immunogenetics 51:289-95).	Infection and inflammation such as inflammatory bowel disease, gluten-sensitive enteropathy, and urinary tract infection)
sbg103302 6C1q	An embodiment of the invention is the use of sbg1033026C1q to regulate central nervous system functions. A close homologue of sbg1033026C1q is C1q-related factor. C1q is a subunit of the C1 enzyme complex that activates the serum complement system. It has been shown that human C1q-related factor (CRF) transcript is expressed at highest levels in the brain, particularly in the brainstem. Similarly, in mouse brain CRF transcripts are most abundant in areas of the nervous system involved in motor function (Berube NG, Swanson XH, Bertram MJ, Kittle JD, Didenko V, Baskin DS, Smith JR, and Pereira-Smith OM., 1999, Brain Res. Mol. Brain Res. 63:233-240). Moreover, ACRP30 is structurally similar to complement factor C1q, and it forms large homooligomers that undergo a series of post-translational modifications. ACRP30 proteins may be a factor that participates in the complex balanced system of energy homeostasis involving food intake, carbohydrate catabolism, and lipid catabolism (Scherer PE, Williams S, Fogliano M, Baldini G, Lodish HF; 1995; J Biol Chem 270:26746-9).	Central nervous system disorder
sbg100367 5RNase	An embodiment of the invention is the use of sbg1003675RNase as a promising tool for anticancer therapy, and apoptosis-related disorders. A close homologue of sbg1003675RNase is RNase. It has been shown that a genetic-engineered pancreatic RNase has cytotoxic action on mouse and human tumor cells, but lacks any appreciable	Viral infection, and tumor

	<p>toxicity on human and mouse normal cells. This variant of human pancreatic RNase selectively sensitized cells derived from a human thyroid tumor to apoptotic death. Because of its selectivity for tumor cells, and because of its human origin, this protein was thought to represent a promising tool for anticancer therapy (Piccoli R, Di Gaetano S, De Lorenzo C, Grauso M, Monaco C, Spalletti-Cernia D, Laccetti P, Cinatl J, Matousek J, D'Alessio G. 1999. Proc Natl Acad Sci U S A 96:7768-73). Moreover, RNase itself can be used to treat an RNA viral infection, and its antagonist of this RNase may be useful in treating apoptosis-related disorders.</p>	
<p>sbg101525 8PLM</p>	<p>An embodiment of the invention is the use of sbg1015258PLM to regulate skeletal and cardiac muscle disorders. A close homologue of sbg1015258PLM is phospholemman. The phospholemman (PLM) is enriched in skeletal muscle and the heart, and is a major substrate phosphorylated in response to insulin and adrenergic stimulation. All phospholemman proteins are small and have a single transmembrane domain (Chen LS, Lo CF, Numann R, Cuddy M. 1997. Genomics 41:435-4). Phospholemman can be phosphorylated by protein kinases A and C to induce a hyperpolarization-activated chloride current, and therefore may play a role in muscle contraction. Recently phospholemman was shown to be a substrate for myotonic dystrophy protein kinase, and therefore is associated with the disease, an autosomal dominant-inherited disorder with prominent effects on skeletal and cardiac muscle (Mounsey JP, John JE 3rd, Helmke SM, Bush EW, Gilbert J, Roses AD, Perryman MB, Jones LR, Moorman JR. 2000. J Biol Chem ;275:23362-7).</p>	<p>Myotonic muscular dystrophy</p>
<p>sbg100332 8IG</p>	<p>An embodiment of the invention is the use of sbg1003328IG to generate immunosuppressants to suppress immune responses. A close homologue of sbg1003328IG is V7, a human leukocyte surface protein (Stockinger H, Gadd SJ, Eher R, Majdic O, Schreiber W, Kasinrerker W, Strass B, Schnabl E, Knapp W. 1990. J Immunol 145:3889-97). sbg1003328IG is an immunoglobulin (Ig)-like membrane protein containing three potential Ig domains, and it has an overall strong sequence similarity to V7.</p>	<p>Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation</p>
<p>sbg102082 9SGLT</p>	<p>An embodiment of the invention is the use of sbg1020829SGLT to regulate Na(+)-dependent glucose transport. A close homologue of sbg1020829SGLT is Na+/glucose cotransporters. The human intestinal Na+/glucose cotransporter (SGLT1) was cloned and sequenced. Close homology was observed between the human and rabbit intestinal Na+/glucose cotransporters, and a significant homology was found between these and the Escherichia coli Na+/proline cotransporter (putP) indicating that the mammalian Na+/glucose and prokaryote Na+/proline cotransporters sharing a common ancestral gene (Hediger MA, Turk E, Wright EM. 1989 Proc Natl Acad Sci U S A Aug;86(15):5748-52). In addition, study of intestinal biopsies of glucose/galactose malabsorption (GCM) patients has revealed a specific defect in Na(+)-dependent absorption of glucose in the brush border. A single missense mutation was found in SGLT1 amplified from the genomic DNA derived from members of a family affected with GGM. This mutated SGLT1 cosegregated with the GGM</p>	<p>Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation and glucose/galactose malabsorption</p>

	phenotype and resulted in a complete loss of Na(+)-dependent glucose transport in <i>Xenopus</i> oocytes injected with this complementary RNA (Turk E, Zabel B, Mundlos S, Dyer J, Wright EM. 1991 Nature Mar 28;350(6316):354-6).	
sbg100545 UDPGT	An embodiment of the invention is the use of sbg100545UDPGT to regulate estrogen and androgen catabolism in peripheral steroid target tissues. A close homologue of sbg100545UDPGT is UDP-glucuronosyltransferase (UDPGT) gene. Mutations had been found in the promoter and coding regions of UDP-glucuronosyltransferase (UDPGT) gene in seven patients with Crigler-Najjar syndrome type II caused by reduction in hepatic bilirubin UDPGT activity (Yamamoto K, Soeda Y, Kamisako T, Hosaka H, Fukano M, Sato H, Fujiyama Y, Adachi Y, Satoh Y, Bamba T. 1998. J Hum Genet 43(2):111-4). A case of Gilbert syndrome caused by a homozygous missense mutation of the bilirubin UDPGT gene was also reported (Maruo Y, Sato H, Yamano T, Doida Y, Shimada M. 1998. J Pediatr Jun;132(6):1045-7). In addition, monkey UDPGT UGT1A9 had been cloned and the mRNA was expressed in extrahepatic estrogen-responsive tissues indicating its potential role in estrogen metabolism (Albert C, Vallee M, Beaudry G, Belanger A, Hum DW. 1999. Endocrinology Jul;140(7):3292-302). Human UDPGT UGT2B23 transcript was also expressed in extrahepatic tissues including prostate, mammary gland, epididymis, testis, and ovary. The activity of UGT2B23 was tested with 62 potential endogenous substrates and was demonstrated to be active on 6 steroids and the bile acid, hyodeoxycholic acid suggesting that UGT2B23 might play an important role in estrogen and androgen catabolism in peripheral steroid target tissues (Barbier O, Levesque E, Belanger A, Hum DW. 1999. Endocrinology Dec;140(12):5538-48).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, Gilbert syndrome, Crigler-Najjar syndrome (CN) type II, and steroid hormone catabolism malfunction
sbg100262 OTIa	An embodiment of the invention is the use of sbg100262OTIa to regulate human tumor cells. A close homologue of sbg100262OTIa is human hypothetical protein DKFZp434B044. This gene is also similar to trypsin inhibitor which contains Sc7 family of extracellular domains at its N-terminal region (Genome Res. 11 (3), 422-435 (2001)). Trypsin inhibitor P25TI sequence had similarity to CRISP family proteins including insect venom allergens, mammalian testis-specific proteins and plant pathogenesis-related proteins. mRNA encoding P25TI and another two glioma pathogenesis-related protein GliPR and RTVP-1, which were also shown to be structurally similar to CRISP family proteins was frequently expressed in human tumor tissues but not detected in normal human tissue cell lines (Yamakawa T, Miyata S, Ogawa N, Koshikawa N, Yasumitsu H, Kanamori T, Miyazaki K 1998. Biochim Biophys Acta Jan 21; 1395(2):202-8., Murphy EV, Zhang Y, Zhu W, Biggs J. 1995. Gene Jun 14;159(1):131-5., Rich T, Chen P, Furman F, Huynh N, Israel MA. 1996. Gene Nov 21;180(1-2):125-30).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, blood coagulation disorders, cellular adhesion disorders, pancreatitis, shock, multi-organ failure, and gastrointestinal ulceration
sbg100262 OTIb	An embodiment of the invention is the use of sbg100262OTIb as a marker for some nervous system tumors, and to regulate expression of human neuroblastoma and glioblastoma. A close homologue of sbg100262OTIb is late-gestation lung 1 (LGL1) protein. Late-gestation lung 1 (LGL1) protein showed 81% homology to P25TI, the trypsin	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders,

	<p>inhibitor purified from the culture medium of human glioblastoma cells (Kaplan F, Ledoux P, Kassamali FQ, Gagnon S, Post M, Koehler D, Deimling J, Sweezey NB. 1999. <i>Am J Physiol</i> Jun;276(6 Pt 1):L1027-36; Koshikawa N, Nakamura T, Tsuchiya N, Isaji M, Yasumitsu H, Umeda M, Miyazaki K. 1996. <i>J Biochem (Tokyo)</i> Feb;119(2):334-9). The cDNA encoding P2STI was isolated and the sequence had similarity to CRISP family proteins including insect venom allergens, mammalian testis-specific proteins and plant pathogenesis-related proteins. P2STI mRNA was frequently expressed in human neuroblastoma and glioblastoma but not detected in normal human tissues cell lines (Yamakawa T, Miyata S, Ogawa N, Koshikawa N, Yasumitsu H, Kanamori T, Miyazaki K. 1998. <i>Biochim Biophys Acta</i> Jan 21; 1395(2):202-8). Another two glioma pathogenesis-related protein GliPR and RTVP-1 were also shown to be structurally similar to CRISP family proteins. The GLIPR gene was highly expressed in the human brain tumor, glioblastoma multiforme/astrocytoma, but neither in normal fetal or adult brain tissue, nor in other nervous system tumors (Murphy EV, Zhang Y, Zhu W, Biggs J. 1995. <i>Gene</i> Jun 14;159(1):131-5). Multiple RTVP-1 mRNA species were highly expressed in a panel of cell lines from nervous system tumors arising from glia, in contrast, the expression of these RNAs was low or absent in nonglial-derived nervous system tumor cell lines (Rich T, Chen P, Furman F, Huynh N, Israel MA. 1996. <i>Gene</i> Nov 21;180(1-2):125-30).</p>	<p>inflammation, blood coagulation disorders, cellular adhesion disorders, pancreatitis, shock, multi-organ failure, and gastrointestinal ulceration</p>
<p>sbg102200 MCTa</p>	<p>An embodiment of the invention is the use of sbg102200MCTa in regulating cancer cells, including the hematopoietic lineages, Burkitt's lymphoma, and solid tumor cells. A close homologue of sbg102200MCTa is MCT1 from Chinese hamster and mouse. Mouse H⁺-monocarboxylate cotransporter (MCT1) was cloned and sequenced from Ehrlich Lettre tumour cells, the sequence of MCT1 is 93% and 87% homologous to MCT1 from Chinese hamster and human, respectively. N-glycanase-F treatment and an in vitro translation experiments demonstrated that glycosylation was not required for MCT1 function (Carpenter L, Poole RC, Halestrap AP. 1996. <i>Biochim Biophys Acta</i> Mar 13;1279(2):157-63). Chick monocarboxylate transporter MCT3 cloned from retinal pigment epithelium (RPE) cDNA library was found only expressed in RPE cells. A rat thyroid epithelial cell line FRTL transfected with pCI-neo/MCT3 showed enhanced pyruvate uptake suggesting that MCT3 may regulate lactate levels in the interphotoreceptor space (Yoon H, Fanelli A, Grollman EF, Philp NJ. 1997. <i>Biochem Biophys Res Commun</i> May 8;234(1):90-4). In human, MCT2 had been implicated as a primary pyruvate transporter in man. The mRNAs of MCT1 and MCT2 were found co-expressed in various human cancer cell lines, including the hematopoietic lineages HL60, K562, MOLT-4, Burkitt's lymphoma Raji, and solid tumor cells such as SW480, A549, and G361. These findings suggested that human MCT1 and MCT2 may have distinct biological roles (Lin RY, Vera JC, Chaganti RS, Golde DW. 1998. <i>J Biol Chem</i> Oct 30;273(44):28959-65).</p>	<p>Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation</p>
<p>sbg102200 MCTb</p>	<p>An embodiment of the invention is the use of sbg102200MCTb in regulating cancer cells, including the hematopoietic lineages, Burkitt's lymphoma, and solid tumor</p>	<p>Cancer, infection, autoimmune disorder,</p>

	<p>cells. A close homologue of sbg102200MCTb is MCT1 from Chinese hamster and mouse. Mouse H⁺-monocarboxylate cotransporter (MCT1) was cloned and sequenced from Ehrlich Lettre tumour cells, the sequence of MCT1 is 93% and 87% homologous to MCT1 from Chinese hamster and human, respectively. N-glycanase-F treatment and an in vitro translation experiments demonstrated that glycosylation was not required for MCT1 function (Carpenter L, Poole RC, Halestrap AP. 1996. <i>Biochim Biophys Acta</i> Mar 13;1279(2):157-63). Chick monocarboxylate transporter MCT3 cloned from retinal pigment epithelium (RPE) cDNA library was found only expressed in RPE cells. A rat thyroid epithelial cell line FRTL transfected with pCI-neo/MCT3 showed enhanced pyruvate uptake suggesting that MCT3 may regulate lactate levels in the interphotoreceptor space (Yoon H, Fanelli A, Grollman EF, Philp NJ. 1997. <i>Biochem Biophys Res Commun</i> May 8;234(1):90-4). In human, MCT2 had been implicated as a primary pyruvate transporter in man. The mRNAs of MCT1 and MCT2 were found co-expressed in various human cancer cell lines, including the hematopoietic lineages HL60, K562, MOLT-4, Burkitt's lymphoma Raji, and solid tumor cells such as SW480, A549, and G361. These findings suggested that human MCT1 and MCT2 may have distinct biological roles (Lin RY, Vera JC, Chaganti RS, Golde DW. 1998. <i>J Biol Chem</i> Oct 30;273(44):28959-65).</p>	<p>hematopoietic disorder, wound healing disorders, and inflammation</p>
<p>sbg102038 OLYG</p>	<p>An embodiment of the invention is the use of sbg102038OLYG in the immune system and enhance the activity of immunoagents and may serve as biomarkers of periodontal disease activity. Close homologues of sbg102038OLYG are lysozymes. Lysozymes are bacteriolytic defensive agents and have been adapted to serve a digestive function (Qasba PK, Kumar S, 1997, <i>Crit Rev Biochem Mol Biol</i> 32:255-306). Those in tissue and body fluids are involved in the immune system and enhance the activity of immunoagents. Llysozymes may serve as biomarkers of periodontal disease activity from inflammatory cell origin (Eley BM, and Cox SW, 1998, <i>Br Dent J</i> 184:323-8).</p>	<p>Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation</p>
<p>sbg100702 6SGLT</p>	<p>An embodiment of the invention is the use of sbg1007026SGLT, a human sodium-glucose cotransporter, in regulation of Glucose/galactose malabsorption (GGM), familial renal glycosuria, and diabetic renal disorders. Close homologues of sbg1007026SGLT are other sodium-glucose cotransporters from humans and rabbits. Human sodium-glucose cotransporters are responsible for the active accumulation of glucose in cells (Hediger MA, Turk E, Wright EM. 1989. <i>Proc Natl Acad Sci U S A</i> 86:5748-52). The renal sodium-glucose cotransporter may be related to the pathophysiology of renal diseases such as familial renal glycosuria and diabetic renal disorders (Kanai Y, Lee WS, You G, Brown D, Hediger MA. 1994. <i>J Clin Invest</i> 93:397-404). In addition, study of glucose/galactose malabsorption (GGM) patients has revealed a specific defect in sodium-dependent absorption of glucose in the brush border, and the consequent severe diarrhea and dehydration caused by glucose/galactose malabsorption are usually lethal unless these sugars are eliminated from the diet (Turk E, Zabel B, Mundlos S, Dyer J, Wright EM. 1991 <i>Nature</i> 350:354-6).</p>	<p>Glucose/galactose malabsorption (GGM), familial renal glycosuria, and diabetic renal disorders</p>

sbg101273 2GLUT	<p>An embodiment of the invention is the use of sbg1012732GLUT, in the maintenance of cellular homeostasis and metabolism. Close homologues of sbg1012732GLUT are transmembrane glucose transporters (gluts). Glucose uptake is achieved by transmembrane glucose transporters (gluts), and the transport of glucose across plasma membranes is important for the maintenance of cellular homeostasis and metabolism. Glucose is taken up by cells and then phosphorylated to glucose-6-phosphate, and glucose utilization by cancer cells is greatly enhanced when compared with that by normal tissue. Tumor tissue is frequently associated with the abnormal and/or over-expression of glucose transporters, especially glut1 (Smith TA. 1999. Br J Biomed Sci 56:285-92). Increased utilization of glucose in glomerular cells cause the increased expression and activity of aldose reductase, protein kinase C and TGF-beta, which have been implicated in excessive extracellular matrix accumulation in diabetic nephropathy (Z Katedry i Zakladu Patofizjologii, Akaemii Medycznej w Poznaniu. 1999. Przegl Lek 56:793-9). Changes in endothelial glucose transport and GLUT1 abundance in the barriers of the brain and retina may severely affect glucose delivery to these tissues and major implications in the development of two major diabetic complications, insulin-induced hypoglycemia and diabetic retinopathy (Kumagai AK. 1999. Diabetes Metab Res Rev 15:261-73).</p>	Tumor, diabetic nephropathy, and insulin-induced hypoglycemia
sbg101273 2GLUTb	<p>An embodiment of the invention is the use of sbg1012732GLUTb, in the maintenance of cellular homeostasis and metabolism. Close homologues of sbg1012732GLUTb are transmembrane glucose transporters (gluts). Glucose uptake is achieved by transmembrane glucose transporters (gluts), and the transport of glucose across plasma membranes is important for the maintenance of cellular homeostasis and metabolism. Glucose is taken up by cells and then phosphorylated to glucose-6-phosphate, and glucose utilization by cancer cells is greatly enhanced when compared with that by normal tissue. Tumor tissue is frequently associated with the abnormal and/or over-expression of glucose transporters, especially glut1 (Smith TA. 1999. Br J Biomed Sci 56:285-92). Increased utilization of glucose in glomerular cells cause the increased expression and activity of aldose reductase, protein kinase C and TGF-beta, which have been implicated in excessive extracellular matrix accumulation in diabetic nephropathy (Z Katedry i Zakladu Patofizjologii, Akaemii Medycznej w Poznaniu. 1999. Przegl Lek 56:793-9). Changes in endothelial glucose transport and GLUT1 abundance in the barriers of the brain and retina may severely affect glucose delivery to these tissues and major implications in the development of two major diabetic complications, insulin-induced hypoglycemia and diabetic retinopathy (Kumagai AK. 1999. Diabetes Metab Res Rev 15:261-73).</p>	Tumor, diabetic nephropathy, and insulin-induced hypoglycemia
sbg101817 2CSP	<p>An embodiment of the invention is the use of sbg1018172CSP in regulation of melanoma, autoimmune disorders, hematopoietic disorder, wound healing, and inflammation. A close homologue of sbg1018172CSP is melanoma-associated chondroitin sulfate proteoglycan</p>	Melanoma, infection, autoimmune disorder, hematopoietic

	<p>(MCSP) core protein NG2. The MCSP core protein NG2 can act as a coreceptor for spreading and focal contact formation in association with alpha 4 beta 1 integrin in melanoma cells (Iida J, Meijne AM, Spiro RC, Roos E, Furcht LT, McCarthy JB. 1995. <i>Cancer Res</i> Mar 15;55(10):2177-85). Cloning of MCSP recognized by mAb 9.2.27 showed that the core protein contained an open reading frame of 2322 AAs, encompassing a large extracellular domain, a hydrophobic transmembrane region, and a relatively short cytoplasmic tail. MCSP RNA was detected in human melanoma cell lines and in biopsies prepared from melanoma skin metastases but not in other human cancer cells or a variety of human fetal and adult tissues (Pluschke G, Vanek M, Evans A, Dittmar T, Schmid P, Itin P, Filardo EJ, Reisfeld RA. 1996. <i>Proc Natl Acad Sci U S A</i> Sep 3;93(18):9710-5).</p>	<p>disorder, wound healing, and inflammation</p>
<p>sbg100457 0ERGIC</p>	<p>An embodiment of the invention is the use of sbg1004570ERGIC as a probe for studying protein trafficking in the secretory pathway which is crucial for the elucidation and treatment of many inherited and acquired diseases, such as cystic fibrosis, Alzheimer's disease and viral infections in regulation of melanoma, autoimmune disorders, hematopoietic disorder, wound healing, and inflammation. A close homologue of sbg1004570ERGIC is ERGIC-53, an ER-Golgi intermediate compartment (ERGIC) protein. A ERGIC protein was elevated more than two fold in HT-29 colon adenocarcinoma cells resistant to the the antitumor drug KRN5500. Together with other information, the cellular secretory pathway was suggested a primary determinant of sensitivity to KRN550 (Kamishohara M, Kenney S, Domergue R, Vistica DT, Sausville EA. 2000 <i>Exp Cell Res</i> May 1;256(2):468-79). Mutations in ERGIC-53 was shown to cause combined deficiency of coagulation factors V and VIII and it was suggested that ERGIC-53 might function as a molecular chaperone for the transport from ER to Golgi of a specific subset of secreted proteins, including coagulation factors V and VII (Nichols WC, Seligsohn U, Zivelin A, Terry VH, Hertel CE, Wheatley MA, Moussalli MJ, Hauri HP, Ciavarella N, Kaufman RJ, Ginsburg D. 1998. <i>Cell</i> Apr 3;93(1):61-70). In addition, ERGIC-53 was reviewed as an attractive probe for studying numerous aspects of protein trafficking in the secretory pathway which is crucial for the elucidation and treatment of many inherited and acquired diseases, such as cystic fibrosis, Alzheimer's disease and viral infections (Hauri HP, Kappeler F, Andersson H, Appenzeller C. 2000 <i>J Cell Sci</i> Feb;113 (Pt 4):587-96).</p>	<p>Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, and Alzheimer's disease.</p>
<p>sbg101699 5IGBrecpt</p>	<p>An embodiment of the invention is the use of sbg1016995IGBrecpt in the clearance of circulating autoantibodies and immune complexes. A close homologue of sbg1016995IGBrecpt is guinea pig Fc receptor for immunoglobulin (Tominaga M, Sakata A, Ohmura T, Yamashita T, Koyama J, Onoue K, 1990. <i>Biochem Biophys Res Commun</i> Apr 30;168(2):683-9). IgG Fc-receptor polymorphisms have been reported recently in patients with guillain-Barre syndrome indicating the role of IgG Fc-receptor in the clearance of circulating autoantibodies and immune complexes (Vedeler CA, Raknes G, Myhr KM, Nyland H. 2000 <i>Neurology</i> Sep 12;55(5):705-7).</p>	<p>Auto-immune diseases, allergy, and guillain-Barre syndrom</p>

sbg1151bS REC	<p>An embodiment of the invention is the use of sbg1151bSREC, a scavenger receptor, in the regulation of pathogenesis in atherosclerosis and the formation of foam cells in atherosclerotic lesions. A close homologue of sbg1151bSREC is scavenger receptor class A type I and type II. Most of the scavenger receptors interacted with several structurally different ligands such as oxidized low density lipoprotein (Ox-LDL) and acetyl LDL. Several studies showed Ox-LDL was involved in the pathogenesis of atherosclerosis (Steinbrecher UP. 1999 Biochim Biophys Acta Jan 4;1436(3):279-98). In macrophages scattered in aortic walls without atherosclerotic lesions, scavenger receptor class A type I and type II (SRA) was detected weakly but consistently. In contrast, in atherosclerotic lesions, macrophages around the core region showed a strong immunoreactivity to SRA indicating the involvement of SRA in the formation of foam cells in atherosclerotic lesions (Nakata A, Nakagawa Y, Nishida M, Nozaki S, Miyagawa J, Nakagawa T, Tamura R, Matsumoto K, Kameda-Takemura K, Yamashita S and Matsuzawa Y. Arterioscler Thromb Vasc Biol 1999 May;19(5):1333-9).</p>	Atherosclerosis disease
sbg139985 4ANK	<p>An embodiment of the invention is the use of sbg1399854ANK in protein-protein interactions and it may act by inhibiting protein of cyclin dependent kinase. The present invention contains both death domain and ankyrin repeat region. The death domain is involved in cell death signaling (Cleveland J. and Ihle J.N. 1995. Cell 81:479-482). Ankyrin repeats (ANK) are tandem repeat modules of about 33 amino acids. Many ankyrin repeat regions are known to be involved in protein-protein interaction (Svetlana Gorina and Nikola P. Pavletich; 1996 Science 274:1001-1005).</p>	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation

Table IV. Quantitative, Tissue-specific mRNA expression detected using SybrMan

Quantitative, tissue-specific, mRNA expression patterns of the genes were measured using SYBR-Green Quantitative PCR (Applied Biosystems, Foster City, CA; see Schmittgen T.D. et al., Analytical Biochemistry 285:194-204, 2000) and human cDNAs prepared from various human tissues. Gene-specific PCR primers were designed using the first nucleic acid sequence listed in the Sequence List for each gene. The threshold cycle (C_t) is defined as the fractional cycle number at which the reporter fluorescence generated by cleavage of the probe reaches a threshold defined as 10 times the background. In cases sequence detection system software predicted more than one PCR product, Taqman was used for the specific PCR amplification as indicated under the specific genes.

In each gene's first subset table, two replicate measurements of gene of identification (GOI) mRNA were measured from various human tissues (column 3 and 4). The average GOI mRNA copies of the two replicates were made from each tissue RNA (column 5). The average amount of 18S rRNA from each tissue RNA was measured (column 6) and used for normalization. To make each tissue with the same amount of 50 ng of 18S rRNA, the normalization factor (column 7) was calculated by dividing 50 ng with the amount of 18S rRNA measured from each tissue (column 6). The mRNA copies per 50 ng of total RNA were obtained by multiplying each GOI normalization factor and the average mRNA copies (column 8).

Fold changes shown in each gene's second subset table were only calculated for disease tissues which have a normal counterpart. There are blanks in the fold change column for all samples that do not have counterparts. In addition, the fold change calculations are the fold change in the disease sample as compared to the normal sample. Accordingly, there will not be a fold change calculation next to any of the normal samples. For patient matched cancer pairs (colon, lung, and breast), each tumor is compared to its specific normal counterpart. When patient-matched normal/disease pairs do not exist, each disease sample was compared back to the average of all the normal samples of that same tissue type. For example, normal brain from the same patient that provided Alzheimer's brain is not applicable. Three normal brain samples and 4 Alzheimer's brain samples are used in the fold change. Three normal samples were averaged, and each of the Alzheimer's samples was compared back to that average.

Abbreviations

ALZ Alzheimer's Disease

CT CLONTECH (1020 East Meadow Circle Palo Alto, CA 94303-4230, USA)

KC Sample prepared by GSK investigator

COPD chronic obstructive pulmonary disease

endo endothelial

VEGF vascular endothelial growth factor

bFGF basic fibroblast growth factor

BM bone marrow

osteo osteoblast

OA osteoarthritis

RA rheumatoid arthritis

PBL peripheral blood lymphocytes

PBMNC peripheral blood mononuclear cells

HIV human immunodeficiency virus

HSV Herpes simplex virus

HPV human papilloma virus

Gene Name sbg960509cbrept

Lowest overall expression in normal and disease samples. Highest normal expression in the whole brain, fetal liver, and uterus. Highest disease expression in 2 of the lung tumor samples, one of the breast tumor samples, and one of the normal breast samples. Downregulation in 1 of 4 colon tumors implies an involvement in cancer of the colon. Downregulation in 2 of 4 AD brain samples as well as high expression in whole brain suggests an involvement in Alzheimer's disease. Downregulation in 3 of 3 COPD lung samples and downregulation in 4 of 4 asthmatic lung samples implicates this gene in COPD and asthma. Upregulation in 2 of 3 heart samples proposes roles in non-obstructive and obstructive DCM. Patterns difficult to interpret due to Cts > 35. Moderate to low expression in immune cells. Moderate expression in OA and RA synovium.

Sample sbg960509cbrept	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 40	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	40, 40	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	33.26, 32.07	24.63	48.4	36.52	7.24	6.91	252.18
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	40, 40	0	0	0.00	2.17	23.04	0.00
Cervix	40, 40	0	0	0.00	2.42	20.66	0.00
Colon	40, 40	0	0	0.00	2.71	18.45	0.00
Endometrium	40, 40	0.81	0	0.41	0.73	68.21	27.63
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	40, 40	0	0	0.00	2.58	19.38	0.00
Jejunum	35.56, 34.42	6.66	12.71	9.69	6.60	7.58	73.37
Kidney	40, 40	0	0	0.00	2.12	23.58	0.00
Liver	40, 40	0	0	0.00	1.50	33.33	0.00
Fetal Liver Clontech	33.46, 34.83	14.95	27.51	21.23	10.40	4.81	102.07
Lung	40, 40	0	0	0.00	2.57	19.46	0.00
Mammary Gland Clontech	40, 40	21.94	10.06	16.00	13.00	3.85	61.54
Myometrium	40, 40	0	0	0.00	2.34	21.37	0.00
Omentum	40, 40	0	0	0.00	3.94	12.69	0.00
Ovary	40, 40	0	0	0.00	4.34	11.52	0.00
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	40, 40	0	0	0.00	5.48	9.12	0.00
Placenta Clontech	40, 40	0.39	0	0.20	5.26	9.51	1.85
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 40	0	0	0.00	1.23	40.65	0.00
Salivary Gland	34.79, 40	10.31	0	5.16	7.31	6.84	35.26

Clontech							
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	40, 40	0	0	0.00	4.92	10.16	0.00
Stomach	35.8, 38.29	5.82	1.41	3.62	2.73	18.32	66.21
Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	35.13, 35.08	8.48	8.75	8.62	9.89	5.06	43.55
Thyroid	40, 40	0	0	0.00	2.77	18.05	0.00
Trachea Clontech	35.26, ND	7.9	ND	7.90	9.71	5.15	40.68
Urinary Bladder	40, ND	0	ND	0.00	5.47	9.14	0.00
Uterus	35.09, 33.87	8.67	17.4	13.04	5.34	9.36	122.05
genomic	26.62	1067.33					
b-actin	27.44	670.43					
1.00E+05	19.22	100000					
1.00E+05	19.38	100000					
1.00E+04	22.78	10000					
1.00E+04	20.52	10000					
1.00E+03	26.45	1000					
1.00E+03	27.03	1000					
1.00E+02	30.99	100					
1.00E+02	31.26	100					
1.00E+01	40	0					
1.00E+01	40	0					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg960509cbrept	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detecte d/50 ng total RNA	Sample	Fold Change in Disease Populat ion
colon normal GW98-167	21941	29.42		332.32	colon normal	
colon tumor GW98-166	21940	30.95	66.31	132.62	colon tumor	-2.51
colon normal GW98-178	22080	31.32	53.01	106.02	colon normal	
colon tumor GW98-177	22060	30.57	83.1	166.20	colon tumor	1.57
colon normal GW98-561	23514	31.44	49.16	98.32	colon normal	
colon tumor GW98-560	23513	31.81	39.47	78.94	colon tumor	-1.25
colon normal GW98-894	24691	29.44	164.69	329.38	colon normal	
colon tumor GW98-893	24690	34.42	8.18	16.36	colon tumor	-20.13
lung normal GW98-3	20742	28.04	383.11	766.22	lung normal	

lung tumor GW98-2	20741	34.22	9.19	18.38	lung tumor	-41.69
lung normal GW97-179	20677	30.93	66.74	133.48	lung normal	
lung tumor GW97-178	20676	27.11	667.61	1335.22	lung tumor	10.00
lung normal GW98-165	21922	28.31	323.99	647.98	lung normal	
lung tumor GW98-164	21921	30.92	67.22	134.44	lung tumor	-4.82
lung normal GW98-282	22584	31.76	40.67	81.34	lung normal	
lung tumor GW98-281	22583	29.61	148.67	297.34	lung tumor	3.66
breast normal GW00-392	28750	27.64	487.44	487.44	breast normal	
breast tumor GW00-391	28746	27.47	539.99	1079.98	breast tumor	2.22
breast normal GW00-413	28798	33.36	15.44	15.44	breast normal	
breast tumor GW00-412	28797	30.88	68.84	137.68	breast tumor	8.92
breast normal GW00-235:238	27592-95	34.74	6.73	6.73	breast normal	
breast tumor GW00-231:234	27588-91	33.73	12.41	12.41	breast tumor	1.84
breast normal GW98-621	23656	27.7	469.27	938.54	breast normal	
breast tumor GW98-620	23655	33.1	18.13	36.26	breast tumor	-25.88
brain normal BB99-542	25507	31.46	48.61	97.22	brain normal	
brain normal BB99-406	25509	34.17	9.52	19.04	brain normal	
brain normal BB99-904	25546	35.69	3.79	7.58	brain normal	
brain stage 5 ALZ BB99-874	25502	40	0	0.00	brain stage 5 ALZ	-41.28
brain stage 5 ALZ BB99-887	25503	34.96	5.91	11.82	brain stage 5 ALZ	-3.49
brain stage 5 ALZ BB99-862	25504	33.13	17.82	35.64	brain stage 5 ALZ	-1.16
brain stage 5 ALZ BB99-927	25542	40	0	0.00	brain stage 5 ALZ	-41.28
CT lung KC	normal	29.53	155.88	311.76	CT lung	
lung 26 KC	normal				lung 26	
lung 27 KC	normal	39.2	0.46	0.46	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-104.07
lung 28 KC	COPD	40	0	0.00	lung 28	-104.07
lung 23 KC	COPD	34.81	6.44	6.44	lung 23	-16.16
lung 25 KC	normal	40	0	0.00	lung 25	
asthmatic lung ODO3112	29321	38.99	0.52	0.52	asthmatic lung	-200.14
asthmatic lung ODO3433	29323	33.69	12.65	25.30	asthmatic lung	-4.11
asthmatic lung ODO3397	29322	33.53	13.98	27.96	asthmatic lung	-3.72
asthmatic lung ODO4928	29325	34.27	8.96	17.92	asthmatic lung	-5.81
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		40	0	0.00	endo bFGF	0.00
heart Clontech	normal	35.53	4.19	8.38	heart	
heart (T-1) ischemic	29417	34	10.5	21.00	heart T-1	2.51
heart (T-14) non-obstructive DCM	29422	31.16	58.24	116.48	heart T-14	13.90
heart (T-3399) DCM	29426	28.35	317.67	635.34	heart T-3399	75.82

adenoid GW99-269	26162	31.52	46.93	93.86	adenoid	
tonsil GW98-280	22582	30.82	71.35	142.70	tonsil	
T cells PC00314	28453	34.36	8.47	16.94	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	40	0	0.00	B cells	
dendritic cells 28441		31.52	47.02	94.04	dendritic cells	
neutrophils	28440	36.13	2.91	2.91	neutrophils	
eosinophils	28446	40	0	0.00	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim		40	0	0.00	BM stim	0.00
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		40	0	0.00	chondrocytes	
OA Synovium IP12/01	29462	32.08	33.47	33.47	OA Synovium	
OA Synovium NP10/01	29461	31.43	49.5	99.00	OA Synovium	
OA Synovium NP57/00	28464	30.42	91.04	182.08	OA Synovium	
RA Synovium NP03/01	28466	32.11	32.84	65.68	RA Synovium	
RA Synovium NP71/00	28467	31.07	61.51	123.02	RA Synovium	
RA Synovium NP45/00	28475	36.21	2.78	5.56	RA Synovium	
OA bone (biobank)	29217	31.49	47.85	47.85	OA bone (biobank)	
OA bone Sample 1	J. Emory	30.11	109.44	218.88	OA bone	
OA bone Sample 2	J. Emory	32.6	24.52	49.04	OA bone	
Cartilage (pool)	Normal	32.09	33.26	66.52	Cartilage (pool)	
Cartilage (pool)	OA	33.1	18.07	36.14	Cartilage (pool)	-1.84
PBL uninfected	28441	27.68	474.91	949.82	PBL uninfected	
PBL HIV IIIB	28442	31.76	40.5	81.00	PBL HIV IIIB	-11.73
MRC5 uninfected (100%)	29158	40	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	34.15	9.61	19.22	MRC5 HSV strain F	19.22
W12 cells	29179	40	0	0.00	W12 cells	
Keratinocytes	29180	38.16	0.85	1.70	Keratinocytes	
B-actin control		27.02	707.5			
genomic		26.1	1232.73			
1.00E+05		18.64	100000			
1.00E+05		18.95	100000			
1.00E+04		22.4	10000			
1.00E+04		22.17	10000			
1.00E+03		26.34	1000			
1.00E+03		25.94	1000			
1.00E+02		31.03	100			
1.00E+02		32.83	100			
1.00E+01		33.21	10			
1.00E+01		32.93	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg960509cbreapt

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-2.51
colon tumor	1.57
colon tumor	-1.25
colon tumor	-20.13
lung tumor	-41.69
lung tumor	10.00
lung tumor	-4.82
lung tumor	3.66
breast tumor	2.22
breast tumor	8.92
breast tumor	1.84
breast tumor	-25.88
brain stage 5 ALZ	-41.28
brain stage 5 ALZ	-3.49
brain stage 5 ALZ	-1.16
brain stage 5 ALZ	-41.28
lung 24	-104.07
lung 28	-104.07
lung 23	-16.16
asthmatic lung	-200.14
asthmatic lung	-4.11
asthmatic lung	-3.72
asthmatic lung	-5.81
endo VEGF	0.00
endo bFGF	0.00
heart T-1	2.51
heart T-14	13.90
heart T-3399	75.82
BM stim	0.00
osteo undif	0.00
Cartilage (pool)	-1.84
PBL HIV IIIB	-11.73
MRC5 HSV strain F	19.22

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Gene Name sbg614126complfH

- Moderate to low overall expression in normal and disease samples. Highest normal expression in liver and fetal liver. Lower (but still significant expression) is seen in the whole brain, ovary, and uterus. Highest disease expression in 2 of the breast tumor samples, one of the normal brain samples, one of the normal lungs, one of the OA synovium samples, and the HSV-infected MRC5 cells. Upregulation in 1 of 4 colon tumors suggests a role in cancer of the colon. Downregulation in 2 of 4 lung tumors and upregulation in 1 of 4 breast tumors suggest roles in cancers of the lung and breast. Downregulation in 3 of 3 COPD lung samples as well as downregulation in 4 of 4 asthmatic lungs implies an involvement in chronic obstructive pulmonary disease and asthma. Upregulation in 1 of 3 heart samples suggests a role in DCM. Upregulation in HSV implicates involvement in herpes simplex virus as a potential host factor. Moderate to low expression in immune cells, RA and OA synovium bone, and chondrocytes.

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Sample	Ct	Mean	Mean	Average	18S	50	copies
sbg614126complfH	(sample 1)	GOI	GOI	GOI	rRNA	ng/18S	of

	and 2)	copies (sample 1)	copies (sample 2)	Copies	(ng)	rRNA (ng)	mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 40	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	40, 40	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	32.34, 31.88	46.5	61.71	54.11	7.24	6.91	373.65
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	40, 40	0	0	0.00	2.17	23.04	0.00
Cervix	40, 35.04	0	8.88	4.44	2.42	20.66	91.74
Colon	40, 40	0	0	0.00	2.71	18.45	0.00
Endometrium	40, 40	0	0	0.00	0.73	68.21	0.00
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 39.79	0	0.48	0.24	0.32	155.28	37.27
Ileum	40, 36.32	0	4.04	2.02	2.58	19.38	39.15
Jejunum	33.25, 34.19	26.6	14.98	20.79	6.60	7.58	157.50
Kidney	40, 40	0	0	0.00	2.12	23.58	0.00
Liver	28.77, 28.81	417.4	407.38	412.39	1.50	33.33	13746.33
Fetal Liver Clontech	29.63, 29.5	246.38	266.67	256.53	10.40	4.81	1233.29
Lung	40, 40	0	0	0.00	2.57	19.46	0.00
Mammary Gland Clontech	34.19, 40	14.9	0	7.45	13.00	3.85	28.65
Myometrium	35.76, 40	5.7	0	2.85	2.34	21.37	60.90
Omentum	36.04, 33.62	4.81	21.16	12.99	3.94	12.69	164.78
Ovary	34.29, 32.95	14.02	31.93	22.98	4.34	11.52	264.69
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	38.98, 35.35	0.79	7.32	4.06	1.57	31.85	129.14
Parotid Gland	34.58, 33.83	11.74	18.68	15.21	5.48	9.12	138.78
Placenta Clontech	35.73, 35.66	5.82	6.06	5.94	5.26	9.51	56.46
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 40	0.38	0	0.19	1.23	40.65	7.72
Salivary Gland Clontech	40, 40	0.3	0	0.15	7.31	6.84	1.03
Skeletal Muscle Clontech	40, 40	0	0.28	0.14	1.26	39.68	5.56
Skin	40, 40	0	0.33	0.17	1.21	41.32	6.82
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	40, 40	0	0	0.00	4.92	10.16	0.00
Stomach	40, 36	0	4.92	2.46	2.73	18.32	45.05
Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00

Thymus Clontech	40, 37.06	0	2.56	1.28	9.89	5.06	6.47
Thyroid	40, 40	0	0.31	0.16	2.77	18.05	2.80
Trachea Clontech	40, 40	0.28	0	0.14	9.71	5.15	0.72
Urinary Bladder	40, 34.13	0	15.53	7.77	5.47	9.14	70.98
Uterus	33.21, 32.79	27.27	35.32	31.30	5.34	9.36	293.02
genomic	26.93	1288.98					
b-actin	27.55	878.74					
1.00E+05	20.07	100000					
1.00E+05	20.14	100000					
1.00E+04	23.43	10000					
1.00E+04	23.34	10000					
1.00E+03	26.84	1000					
1.00E+03	27.02	1000					
1.00E+02	31.72	100					
1.00E+02	31.32	100					
1.00E+01	33.78	10					
1.00E+01	35.79	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg614126complfH	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detecte d/50 ng total RNA	Sample	Fold Change in Disease Populatio n
colon normal GW98-167	21941	34.6	13.63	27.26	colon normal	
colon tumor GW98-166	21940	35.71	7.35	14.70	colon tumor	-1.85
colon normal GW98-178	22080	40	0	0.00	colon normal	
colon tumor GW98-177	22060	39.81	0.75	1.50	colon tumor	1.50
colon normal GW98-561	23514	38.61	1.45	2.90	colon normal	
colon tumor GW98-560	23513	34.84	11.95	23.90	colon tumor	8.24
colon normal GW98-894	24691	39.05	1.14	2.28	colon normal	
colon tumor GW98-893	24690	40	0	0.00	colon tumor	-2.28
lung normal GW98-3	20742	35.78	7.04	14.08	lung normal	
lung tumor GW98-2	20741	40	0	0.00	lung tumor	-14.08
lung normal GW97-179	20677	33.99	19.21	38.42	lung normal	
lung tumor GW97-178	20676	40	0.49	0.98	lung tumor	-39.20
lung normal GW98-165	21922	39.63	0.82	1.64	lung normal	
lung tumor GW98-164	21921	38.89	1.24	2.48	lung tumor	1.51
lung normal GW98-282	22584	40	0	0.00	lung normal	
lung tumor GW98-281	22583	40	0	0.00	lung tumor	0.00

breast normal GW00-392	28750	32.71	39.28	39.28	breast normal	
breast tumor GW00-391	28746	31.65	70.89	141.78	breast tumor	3.61
breast normal GW00-413	28798	35.83	6.88	6.88	breast normal	
breast tumor GW00-412	28797	33.17	30.3	60.60	breast tumor	8.81
breast normal GW00-235:238	27592-95	36.73	4.16	4.16	breast normal	
breast tumor GW00-231:234	27588-91	35.98	6.33	6.33	breast tumor	1.52
breast normal GW98-621	23656	37.38	2.89	5.78	breast normal	
breast tumor GW98-620	23655	34.95	11.23	22.46	breast tumor	3.89
brain normal BB99-542	25507	32.26	50.34	100.68	brain normal	
brain normal BB99-406	25509	40	0.57	1.14	brain normal	
brain normal BB99-904	25546	34.68	13.04	26.08	brain normal	
brain stage 5 ALZ BB99-874	25502	40	0	0.00	brain stage 5 ALZ	-42.63
brain stage 5 ALZ BB99-887	25503	35.87	6.73	13.46	brain stage 5 ALZ	-3.17
brain stage 5 ALZ BB99-862	25504	39.2	1.05	2.10	brain stage 5 ALZ	-20.30
brain stage 5 ALZ BB99-927	25542	40	0	0.00	brain stage 5 ALZ	-42.63
CT lung KC	normal	39.4	0.93	1.86	CT lung	
lung 26 KC	normal				lung 26	
lung 27 KC	normal	40	0	0.00	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-0.62
lung 28 KC	COPD	40	0	0.00	lung 28	-0.62
lung 23 KC	COPD	40	0	0.00	lung 23	-0.62
lung 25 KC	normal	40	0	0.00	lung 25	
asthmatic lung ODO3112	29321	36.52	4.68	4.68	asthmatic lung	7.55
asthmatic lung ODO3433	29323	40	0	0.00	asthmatic lung	-0.62
asthmatic lung ODO3397	29322	40	0	0.00	asthmatic lung	-0.62
asthmatic lung ODO4928	29325	38.18	1.85	3.70	asthmatic lung	5.97
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		40	0	0.00	endo bFGF	0.00
heart Clontech	normal	40	0	0.00	heart	
heart (T-1) ischemic	29417	40	0	0.00	heart T-1	0.00
heart (T-14) non-obstructive DCM	29422	40	0	0.00	heart T-14	0.00
heart (T-3399) DCM	29426	36.03	6.13	12.26	heart T-3399	12.26
adenoid GW99-269	26162	34.08	18.19	36.38	adenoid	
tonsil GW98-280	22582	37.46	2.77	5.54	tonsil	
T cells PC00314	28453	40	0	0.00	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	

B cells PC00665	28455	34.56	13.99	27.98	B cells	
dendritic cells 28441		40	0	0.00	dendritic cells	
neutrophils	28440	33.76	21.85	21.85	neutrophils	
eosinophils	28446	40	0	0.00	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim		40	0	0.00	BM stim	0.00
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		34.25	16.55	41.38	chondrocytes	
OA Synovium IP12/01	29462	40	0	0.00	OA Synovium	
OA Synovium NP10/01	29461	40	0	0.00	OA Synovium	
OA Synovium NP57/00	28464	33.1	31.54	63.08	OA Synovium	
RA Synovium NP03/01	28466	40	0	0.00	RA Synovium	
RA Synovium NP71/00	28467	40	0	0.00	RA Synovium	
RA Synovium NP45/00	28475	40	0	0.00	RA Synovium	
OA bone (biobank)	29217	40	0	0.00	OA bone (biobank)	
OA bone Sample 1	J. Emory	40	0	0.00	OA bone	
OA bone Sample 2	J. Emory	40	0	0.00	OA bone	
Cartilage (pool)	Normal	40	0	0.00	Cartilage (pool)	
Cartilage (pool)	OA	40	0	0.00	Cartilage (pool)	0.00
PBL uninfected	28441	36.12	5.84	11.68	PBL uninfected	
PBL HIV IIIB	28442	36.1	5.9	11.80	PBL HIV IIIB	1.01
MRC5 uninfected (100%)	29158	40	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	31.83	64.08	128.16	MRC5 HSV strain F	128.16
W12 cells	29179	40	0	0.00	W12 cells	
Keratinocytes	29180	40	0	0.00	Keratinocytes	
B-actin control		27.26	820.77			
genomic		26.18	1496.25			
1.00E+05		19.13	100000			
1.00E+05		19.38	100000			
1.00E+04		22.56	10000			
1.00E+04		22.67	10000			
1.00E+03		26.01	1000			
1.00E+03		26.44	1000			
1.00E+02		30.93	100			
1.00E+02		30.1	100			
1.00E+01		38.59	10			
1.00E+01		33.26	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg614126complfH

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.85
colon tumor	1.50
colon tumor	8.24
colon tumor	-2.28
lung tumor	-14.08
lung tumor	-39.20
lung tumor	1.51
lung tumor	0.00
breast tumor	3.61
breast tumor	8.81
breast tumor	1.52
breast tumor	3.89
brain stage 5 ALZ	-42.63
brain stage 5 ALZ	-3.17
brain stage 5 ALZ	-20.30
brain stage 5 ALZ	-42.63
lung 24	-0.62
lung 28	-0.62
lung 23	-0.62
asthmatic lung	7.55
asthmatic lung	-0.62
asthmatic lung	-0.62
asthmatic lung	5.97
endo VEGF	0.00
endo bFGF	0.00
heart T-1	0.00
heart T-14	0.00
heart T-3399	12.26
BM stim	0.00
osteo undif	0.00
Cartilage (pool)	0.00
PBL HIV IIIB	1.01
MRC5 HSV strain F	128.16

Gene Name sbg120703RNase

- 5 Moderate to low overall expression in normal and disease samples. Highest normal expression in whole brain and salivary gland. Moderate expression in the fetal liver and the thymus. Highest disease expression in 2 of the normal lung samples, one of the lung tumor samples, the normal cartilage pool, and the HSV-infected MRC5 cells. Upregulation in 1 of 4 colon tumors suggests a role in cancer of the colon. Downregulation in 2 of 4 lung tumor samples suggests possible
- 10 implication in lung cancer. Upregulation in 2 of 4 breast tumors implies an involvement in cancers of the breast. Downregulation in 3 of 3 COPD lung samples implies an involvement in COPD. Upregulation in 3 of 3 heart samples implicates this gene in diseases of the heart such as DCM and ischemia. High expression in the OA and RA synovium and the OA bone samples suggests a possible involvement in osteoarthritis and rheumatoid arthritis. Upregulation in HSV implicates this
- 15 gene in herpes simplex virus as a potential host factor. Moderate to low expression in immune cells.

Sample sbg120703RNase	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Averag e GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 36.24	0	2.54	1.27	3.06	16.34	20.75
Subcutaneous Adipose Zenbio	36.58, 40	2.07	0	1.04	0.96	52.36	54.19
Adrenal Gland Clontech	40, 40	0.22	0	0.11	0.61	81.97	9.02
Whole Brain Clontech	28.62, 28.6	245.21	247.41	246.31	7.24	6.91	1701.04
Fetal Brain Clontech	40, 40	0.3	0	0.15	0.48	103.95	15.59
Cerebellum Clontech	40, 40	0.29	0	0.15	2.17	23.04	3.34
Cervix	35.3, 40	4.45	0	2.23	2.42	20.66	45.97
Colon	40, 40	0.26	0	0.13	2.71	18.45	2.40
Endometrium	40, 38.38	0	0.7	0.35	0.73	68.21	23.87
Esophagus	36.11, 37.01	2.74	1.6	2.17	1.37	36.50	79.20
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	39.31, 36.07	0.4	2.8	1.60	2.58	19.38	31.01
Jejunum	34.13, 39.51	8.98	0.36	4.67	6.60	7.58	35.38
Kidney	40, 40	0.48	0	0.24	2.12	23.58	5.66
Liver	34.4, 36.04	7.64	2.86	5.25	1.50	33.33	175.00
Fetal Liver Clontech	31.46, 31.39	44.65	46.4	45.53	10.40	4.81	218.87
Lung	34.21, 35.61	8.59	3.71	6.15	2.57	19.46	119.65
Mammary Gland Clontech	34.9, 35.65	5.67	3.6	4.64	13.00	3.85	17.83
Myometrium	40, 38.99	0	0.49	0.25	2.34	21.37	5.24
Omentum	38.39, 34.35	0.7	7.89	4.30	3.94	12.69	54.51
Ovary	35, 33.21	5.34	15.64	10.49	4.34	11.52	120.85
Pancreas	40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	32.22, 33.49	28.28	13.18	20.73	5.48	9.12	189.14
Placenta Clontech	37, 39.59	1.6	0.34	0.97	5.26	9.51	9.22
Prostate	35.03, 35.75	5.23	3.4	4.32	3.00	16.67	71.92
Rectum	38.25, 40	0.76	0.21	0.49	1.23	40.65	19.72
Salivary Gland Clontech	30.01, 29.73	106.25	125.78	116.02	7.31	6.84	793.54
Skeletal Muscle Clontech	40, 39.16	0.41	0.44	0.43	1.26	39.68	16.87
Skin	37.21, 35.01	1.42	5.31	3.37	1.21	41.32	139.05
Small Intestine Clontech	40, 40	0	0.19	0.10	0.98	51.07	4.85
Spleen	35.4, 35.9	4.2	3.11	3.66	4.92	10.16	37.14
Stomach	36.12, 40	2.73	0.21	1.47	2.73	18.32	26.92
Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00

Thymus Clontech	31.88, 31.42	34.61	45.62	40.12	9.89	5.06	202.81
Thyroid	40, 35.22	0	4.67	2.34	2.77	18.05	42.15
Trachea Clontech	35.38, 37.52	4.26	1.17	2.72	9.71	5.15	13.98
Urinary Bladder	38.77, 40	0.56	0.31	0.44	5.47	9.14	3.98
Uterus	33.66, 37.55	11.93	1.16	6.55	5.34	9.36	61.28
genomic	25.78	1342.66					
b-actin	27.27	551.42					
1.00E+05	19.03	100000					
1.00E+05	19.08	100000					
1.00E+04	22.28	10000					
1.00E+04	22.27	10000					
1.00E+03	25.85	1000					
1.00E+03	25.6	1000					
1.00E+02	30.44	100					
1.00E+02	29.33	100					
1.00E+01	34.4	10					
1.00E+01	34.48	10					
1.00E-00							
1.00E-00							
NTC	40	-1					
NTC	40	0					

Sample sbg120703RNase	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detected/ 50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	29.03	142.85	285.70	colon normal	
colon tumor GW98-166	21940	28.31	226.87	453.74	colon tumor	1.59
colon normal GW98-178	22080	33.08	10.78	21.56	colon normal	
colon tumor GW98-177	22060	29.33	118.09	236.18	colon tumor	10.95
colon normal GW98-561	23514	30.02	76.09	152.18	colon normal	
colon tumor GW98-560	23513	30.42	58.89	117.78	colon tumor	-1.29
colon normal GW98-894	24691	29.07	139.29	278.58	colon normal	
colon tumor GW98-893	24690	30.3	63.5	127.00	colon tumor	-2.19
lung normal GW98-3	20742	26.86	574.4	1148.80	lung normal	
lung tumor GW98-2	20741	30.07	73.89	147.78	lung tumor	-7.77
lung normal GW97-179	20677	29.74	90.79	181.58	lung normal	
lung tumor GW97-178	20676	27.63	351.24	702.48	lung tumor	3.87
lung normal GW98-165	21922	26.63	663.94	1327.88	lung normal	
lung tumor GW98-164	21921	29.38	114.52	229.04	lung tumor	-5.80
lung normal GW98-282	22584	30	77.02	154.04	lung normal	
lung tumor GW98-281	22583	29.64	97.04	194.08	lung tumor	1.26
breast normal GW00-392	28750	29.08	138.57	138.57	breast normal	
breast tumor GW00-391	28746	28.77	169.53	339.06	breast tumor	2.45
breast normal GW00-413	28798	32.72	13.55	13.55	breast normal	
breast tumor GW00-412	28797	31.01	40.4	80.80	breast tumor	5.96

breast normal GW00-235:238	27592-95	34.39	4.68	4.68	breast normal	
breast tumor GW00-231:234	27588-91	31.4	31.48	31.48	breast tumor	6.73
breast normal GW98-621	23656	28.54	195.6	391.20	breast normal	
breast tumor GW98-620	23655	30.37	60.84	121.68	breast tumor	-3.21
brain normal BB99-542	25507	32.94	11.79	23.58	brain normal	
brain normal BB99-406	25509	32.22	18.66	37.32	brain normal	
brain normal BB99-904	25546	32.3	17.71	35.42	brain normal	
brain stage 5 ALZ BB99-874	25502	32.82	12.76	25.52	brain stage 5 ALZ	-1.26
brain stage 5 ALZ BB99-887	25503	30.31	63.18	126.36	brain stage 5 ALZ	3.94
brain stage 5 ALZ BB99-862	25504	31.42	31.08	62.16	brain stage 5 ALZ	1.94
brain stage 5 ALZ BB99-927	25542	33.35	9.08	18.16	brain stage 5 ALZ	-1.77
CT lung KC	normal	30.41	59.49	118.98	CT lung	
lung 26 KC	normal				lung 26	
lung 27 KC	normal	37.69	0.57	0.57	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-40.17
lung 28 KC	COPD	40	0	0.00	lung 28	-40.17
lung 23 KC	COPD	40	0	0.00	lung 23	-40.17
lung 25 KC	normal	36.86	0.97	0.97	lung 25	
asthmatic lung ODO3112	29321	33.08	10.79	10.79	asthmatic lung	-3.72
asthmatic lung ODO3433	29323	29.94	80.31	160.62	asthmatic lung	4.00
asthmatic lung ODO3397	29322	29.79	87.94	175.88	asthmatic lung	4.38
asthmatic lung ODO4928	29325	30.08	73.39	146.78	asthmatic lung	3.65
endo cells KC	control	40	0.13	0.13	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	-0.13
endo bFGF KC		40	0.12	0.12	endo bFGF	-1.08
heart Clontech	normal	34.66	3.95	7.90	heart	
heart (T-1) ischemic	29417	30.43	58.48	116.96	heart T-1	14.81
heart (T-14) non-obstructive DCM	29422	30.3	63.76	127.52	heart T-14	16.14
heart (T-3399) DCM	29426	31.14	37.27	74.54	heart T-3399	9.44
adenoid GW99-269	26162	33.15	10.31	20.62	adenoid	
tonsil GW98-280	22582	30.26	65.22	130.44	tonsil	
T cells PC00314	28453	33.29	9.45	18.90	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	32.25	18.35	36.70	B cells	
dendritic cells 28441		30.52	55.34	110.68	dendritic cells	
neutrophils	28440	31.61	27.61	27.61	neutrophils	
eosinophils	28446	33.2	10.01	20.02	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim		40	0	0.00	BM stim	0.00
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		29.65	96.25	240.63	chondrocytes	

OA Synovium IP12/01	29462	28.59	190.09	190.09	OA Synovium	
OA Synovium NP10/01	29461	29.06	140.66	281.32	OA Synovium	
OA Synovium NP57/00	28464	28.38	216.61	433.22	OA Synovium	
RA Synovium NP03/01	28466	29.43	111	222.00	RA Synovium	
RA Synovium NP71/00	28467	28.35	220.48	440.96	RA Synovium	
RA Synovium NP45/00	28475	28.7	176.79	353.58	RA Synovium	
OA bone (biobank)	29217	30.6	52.6	52.60	OA bone (biobank)	
OA bone Sample 1	J. Emory	29.64	97.1	194.20	OA bone	
OA bone Sample 2	J. Emory	30.85	44.71	89.42	OA bone	
Cartilage (pool)	Normal	28.07	264.86	529.72	Cartilage (pool)	
Cartilage (pool)	OA	30.47	56.97	113.94	Cartilage (pool)	-4.65
PBL uninfected	28441	33.41	8.73	17.46	PBL uninfected	
PBL HIV IIIB	28442	32.1	20.17	40.34	PBL HIV IIIB	2.31
MRC5 uninfected (100%)	29158	31.09	38.5	77.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	28.24	237.46	474.92	MRC5 HSV strain F	6.17
W12 cells	29179	28.83	162.45	324.90	W12 cells	
Keratinocytes	29180	29.21	127.89	255.78	Keratinocytes	
B-actin control		26.99	528.52			
genomic		25.66	1229.15			
1.00E+05		18.76	100000			
1.00E+05		19.03	100000			
1.00E+04		22.01	10000			
1.00E+04		22.05	10000			
1.00E+03		26.01	1000			
1.00E+03		25.68	1000			
1.00E+02		30.57	100			
1.00E+02		30.32	100			
1.00E+01		32.24	10			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg120703RNase

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.59
colon tumor	10.95
colon tumor	-1.29
colon tumor	-2.19
lung tumor	-7.77

lung tumor	3.87
lung tumor	-5.80
lung tumor	1.26
breast tumor	2.45
breast tumor	5.96
breast tumor	6.73
breast tumor	-3.21
brain stage 5 ALZ	-1.26
brain stage 5 ALZ	3.94
brain stage 5 ALZ	1.94
brain stage 5 ALZ	-1.77
lung 24	-40.17
lung 28	-40.17
lung 23	-40.17
asthmatic lung	-3.72
asthmatic lung	4.00
asthmatic lung	4.38
asthmatic lung	3.65
endo VEGF	-0.13
endo bFGF	-1.08
heart T-1	14.81
heart T-14	16.14
heart T-3399	9.44
BM stim	0.00
osteo undif	0.00
Cartilage (pool)	-4.65
PBL HIV IIIB	2.31
MRC5 HSV strain F	6.17

Gene Name sbg98530TS

- 5 Moderate overall expression in normal and disease samples. Highest normal expression in whole brain, endometrium, and testis. Moderate expression in normal heart, skeletal muscle, and esophagus. Shows expression in most of the GI tract samples as well as the female reproductive tract samples. Highest disease expression in one of the colon tumor samples, all 3 of the heart samples, and the chondrocytes. Data predominantly shows a muscle-specific pattern of expression.
- 10 Upregulation in 1 of 4 colon tumors and upregulation in 2 of 4 breast tumors implies an involvement in cancers of the colon and breast. Downregulation in 3 of 3 COPD samples implies a role in chronic obstructive pulmonary disease. Downregulation in HSV implicates involvement in herpes simplex virus as a potential host factor. Moderate to low overall expression in immune cells. High expression in chondrocytes and OA and RA synovium suggests possible involvement in osteoarthritis and rheumatoid arthritis.

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Sample sbg98530TS	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 36.35	0	4.22	2.11	3.06	16.34	34.48
Subcutaneous Adipose Zenbio	35.78, 40	5.89	0	2.95	0.96	52.36	154.19
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00

Whole Brain Clontech	26.63, 26.42	1253.02	1414.2	1333.61	7.24	6.91	9210.01
Fetal Brain Clontech	40, 37.33	0	2.38	1.19	0.48	103.95	123.70
Cerebellum Clontech	35.9, 40	5.5	0	2.75	2.17	23.04	63.36
Cervix	33.47, 34.27	22.86	14.26	18.56	2.42	20.66	383.47
Colon	34.49, 34.05	12.58	16.28	14.43	2.71	18.45	266.24
Endometrium	33.28, 32.94	25.41	31.15	28.28	0.73	68.21	1929.06
Esophagus	33.61, 32.9	21.02	31.85	26.44	1.37	36.50	964.78
Heart Clontech	33.32, 33.03	24.91	29.42	27.17	1.32	37.88	1028.98
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	35.89, 33.37	5.53	24.14	14.84	2.58	19.38	287.50
Jejunum	31.55, 31.42	70.2	75.71	72.96	6.60	7.58	552.69
Kidney	40, 35.5	0	6.96	3.48	2.12	23.58	82.08
Liver	34.29, 33.63	14.07	20.78	17.43	1.50	33.33	580.83
Fetal Liver Clontech	32.16, 32.92	49.02	31.52	40.27	10.40	4.81	193.61
Lung	40, 35.78	0		2.95	2.57	19.46	57.30
Mammary Gland Clontech	31.42, 32.08	75.62	51.54	63.58	13.00	3.85	244.54
Myometrium	32.93, 32.03	31.21	52.84	42.03	2.34	21.37	897.97
Omentum	35.21, 40	8.23	0	4.12	3.94	12.69	52.22
Ovary	35.36, 35.51	7.53	6.89	7.21	4.34	11.52	83.06
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 37.54	0	2.11	1.06	1.57	31.85	33.60
Parotid Gland	31.67, 31.01	65.33	96.46	80.90	5.48	9.12	738.09
Placenta Clontech	33.13, 32.05	27.88	52.3	40.09	5.26	9.51	381.08
Prostate	35.03, 40	9.13	5.22	7.18	3.00	16.67	119.58
Rectum	40, 35.19	0	8.32	4.16	1.23	40.65	169.11
Salivary Gland Clontech	32.41, 34.06	42.32	16.15	29.24	7.31	6.84	199.97
Skeletal Muscle Clontech	33.93, 33.76	17.41	19.28	18.35	1.26	39.68	727.98
Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	34.11	11.73	15.7	13.72	0.98	51.07	700.46
Spleen	36.08, 40	4.94	0.37	2.66	4.92	10.16	26.98
Stomach	40, 40	0	0	0.00	2.73	18.32	0.00
Testis Clontech	35.54, 33.26	6.79	25.83	16.31	0.57	87.87	1433.22
Thymus Clontech	33.66, 34.12	20.35	15.62	17.99	9.89	5.06	90.93
Thyroid	40, 35.46	0	7.12	3.56	2.77	18.05	64.26
Trachea Clontech	32.08, 31.84	51.54	59.21	55.38	9.71	5.15	285.14
Urinary Bladder	34.75, 36.99	10.8	2.91	6.86	5.47	9.14	62.66
Uterus	31.79, 32.2	60.97	47.95	54.46	5.34	9.36	509.93
genomic	26.8	1133.17					
b-actin	27.6	706.62					
1.00E+05	19.53	100000					
1.00E+05	19.54	100000					
1.00E+04	22.8	10000					
1.00E+04	23.02	10000					
1.00E+03	26.14	1000					
1.00E+03	26.59	1000					

1.00E+02	31.41	100				
1.00E+02	30.97	100				
1.00E+01	40	0				
1.00E+01	35.24	10				
1.00E-00	40	0				
1.00E-00	40	0				
NTC	40	0				
NTC	40	0				

Sample sbg98530TS	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detecte d/50 ng total RNA	Sample	Fold Change in Disease Populat ion
colon normal GW98-167	21941	26.26	1792.89	3585.78	colon normal	
colon tumor GW98-166	21940	26.2	1856.22	3712.44	colon tumor	1.04
colon normal GW98-178	22080	27.25	986.8	1973.60	colon normal	
colon tumor GW98-177	22060	26.7	1369.12	2738.24	colon tumor	1.39
colon normal GW98-561	23514	27.55	821.35	1642.70	colon normal	
colon tumor GW98-560	23513	24.64	4748.96	9497.92	colon tumor	5.78
colon normal GW98-894	24691	27.27	971.87	1943.74	colon normal	
colon tumor GW98-893	24690	25.35	3093.47	6186.94	colon tumor	3.18
lung normal GW98-3	20742	27.02	1133.68	2267.36	lung normal	
lung tumor GW98-2	20741	27.26	981.94	1963.88	lung tumor	-1.15
lung normal GW97-179	20677	29.14	315.07	630.14	lung normal	
lung tumor GW97-178	20676	28.15	571.76	1143.52	lung tumor	1.81
lung normal GW98-165	21922	27.86	682.2	1364.40	lung normal	
lung tumor GW98-164	21921	27.45	871.19	1742.38	lung tumor	1.28
lung normal GW98-282	22584	28.12	581.74	1163.48	lung normal	
lung tumor GW98-281	22583	29.32	283.71	567.42	lung tumor	-2.05
breast normal GW00-392	28750	27.85	687.38	687.38	breast normal	
breast tumor GW00-391	28746	26.61	1444.19	2888.38	breast tumor	4.20
breast normal GW00-413	28798	28.43	483.03	483.03	breast normal	
breast tumor GW00-412	28797	25.49	2836.66	5673.32	breast tumor	11.75
breast normal GW00-235:238	27592-95	32.26	48.29	48.29	breast normal	
breast tumor GW00-231:234	27588-91	29.07	328.46	328.46	breast tumor	6.80
breast normal GW98-621	23656	26.82	1279.07	2558.14	breast normal	
breast tumor GW98-620	23655	26.8	1289.27	2578.54	breast tumor	1.01
brain normal BB99-542	25507	29.03	337.63	675.26	brain normal	
brain normal BB99-406	25509	29.19	305.6	611.20	brain normal	
brain normal BB99-904	25546	30.44	144.55	289.10	brain normal	
brain stage 5 ALZ BB99-874	25502	28.47	471.8	943.60	brain stage 5 ALZ	1.80
brain stage 5 ALZ BB99-887	25503	27.3	955.52	1911.04	brain stage 5 ALZ	3.64

brain stage 5 ALZ BB99-862	25504	27.42	891.77	1783.54	brain stage 5 ALZ	3.40
brain stage 5 ALZ BB99-927	25542	29.31	285.16	570.32	brain stage 5 ALZ	1.09
CT lung KC	normal	27.96	643.88	1287.76	CT lung	
lung 26 KC	normal	35.82	5.66	5.66	lung 26	
lung 27 KC	normal	40	0	0.00	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-325.52
lung 28 KC	COPD	35.3	7.73	7.73	lung 28	-42.11
lung 23 KC	COPD	36.67	3.39	3.39	lung 23	-96.02
lung 25 KC	normal	35.11	8.67	8.67	lung 25	
asthmatic lung ODO3112	29321	31.01	102.08	102.08	asthmatic lung	-3.19
asthmatic lung ODO3433	29323	29.76	216.81	433.62	asthmatic lung	1.33
asthmatic lung ODO3397	29322	29.83	208.08	416.16	asthmatic lung	1.28
asthmatic lung ODO4928	29325	30.37	150.17	300.34	asthmatic lung	-1.08
endo cells KC	control	37.54	2	2.00	endo cells	
endo VEGF KC		35.77	5.83	5.83	endo VEGF	2.92
endo bFGF KC		40	0	0.00	endo bFGF	-2.00
heart Clontech	normal	26.09	1982.44	3964.88	heart	
heart (T-1) ischemic	29417	24	6956.27	13912.54	heart T-1	3.51
heart (T-14) non-obstructive DCM	29422	24.55	5010.03	10020.06	heart T-14	2.53
heart (T-3399) DCM	29426	24.05	6766.57	13533.14	heart T-3399	3.41
adenoid GW99-269	26162	30.56	134.11	268.22	adenoid	
tonsil GW98-280	22582	27.94	651.01	1302.02	tonsil	
T cells PC00314	28453	29.8	212.45	424.90	T cells	
PBMNC		33.01	30.69	30.69	PBMNC	
monocyte		33.42	23.9	47.80	monocyte	
B cells PC00665	28455	33.52	22.59	45.18	B cells	
dendritic cells 28441		29.07	329.58	659.16	dendritic cells	
neutrophils	28440	30.39	149	149.00	neutrophils	
eosinophils	28446	35.41	7.25	14.50	eosinophils	
BM unstim		34.24	14.65	14.65	BM unstim	
BM stim		36.61	3.51	3.51	BM stim	-4.17
osteo dif		30.55	135.33	135.33	osteo dif	3.02
osteo undif		32.38	44.88	44.88	osteo undif	
chondrocytes		25.35	3089.54	7723.85	chondrocytes	
OA Synovium IP12/01	29462	28.75	398.53	398.53	OA Synovium	
OA Synovium NP10/01	29461	27.04	1119.77	2239.54	OA Synovium	
OA Synovium NP57/00	28464	28.85	375.92	751.84	OA Synovium	
RA Synovium NP03/01	28466	28.14	574.66	1149.32	RA Synovium	
RA Synovium NP71/00	28467	27.58	806.11	1612.22	RA Synovium	
RA Synovium NP45/00	28475	28.04	611.1	1222.20	RA Synovium	
OA bone (biobank)	29217	30.25	161.3	161.30	OA bone (biobank)	
OA bone Sample 1	J. Emory	31.24	89.29	178.58	OA bone	
OA bone Sample 2	J. Emory	30.98	104.34	208.68	OA bone	

Cartilage (pool)	Normal	29.86	204.47	408.94	Cartilage (pool)	
Cartilage (pool)	OA	29.37	275.09	550.18	Cartilage (pool)	1.35
PBL uninfected	28441	26.45	1598.39	3196.78	PBL uninfected	
PBL HIV IIIB	28442	27.57	814.58	1629.16	PBL HIV IIIB	-1.96
MRC5 uninfected (100%)	29158	25.13	3539.95	7079.90	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	30.49	139.89	279.78	MRC5 HSV strain F	-25.31
W12 cells	29179	26.72	1359.04	2718.08	W12 cells	
Keratinocytes	29180	26.41	1633.77	3267.54	Keratinocytes	
B-actin control		27.87	678.8			
genomic		26.9	1214.71			
1.00E+05		19.86	100000			
1.00E+05		19.82	100000			
1.00E+04		23.15	10000			
1.00E+04		23.21	10000			
1.00E+03		26.62	1000			
1.00E+03		26.79	1000			
1.00E+02		31.2	100			
1.00E+02		32.2	100			
1.00E+01		40	0			
1.00E+01		34.53	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg98530TS

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.04
colon tumor	1.39
colon tumor	5.78
colon tumor	3.18
lung tumor	-1.15
lung tumor	1.81
lung tumor	1.28
lung tumor	-2.05
breast tumor	4.20
breast tumor	11.75
breast tumor	6.80
breast tumor	1.01
brain stage 5 ALZ	1.80
brain stage 5 ALZ	3.64
brain stage 5 ALZ	3.40
brain stage 5 ALZ	1.09
lung 24	-325.52
lung 28	-42.11
lung 23	-96.02
asthmatic lung	-3.19
asthmatic lung	1.33

asthmatic lung	1.28
asthmatic lung	-1.08
endo VEGF	2.92
endo bFGF	-2.00
heart T-1	3.51
heart T-14	2.53
heart T-3399	3.41
BM stim	-4.17
osteo undif	3.02
Cartilage (pool)	1.35
PBL HIV IIIB	-1.96
MRC5 HSV strain F	-25.31

Gene Name sbg563917RDP

- 5 Moderate to low overall expression in normal and disease samples. Highest normal expression in testis liver, trachea, and whole brain. Shows good expression in most of the GI tract samples. Highest disease expression in T cells, B cells, neutrophils, and eosinophils. Upregulation in 1 of 4 breast tumors implies involvement in cancer of the breast. Downregulation in 3 of 3 COPD lungs suggests an involvement in chronic obstructive pulmonary disease. Downregulation in the ischemic heart sample implicates this gene in ischemic heart disease. Downregulation in the VEGF and bFGF-treated endothelial cells suggests a role in angiogenesis. Upregulation in HSV implicates involvement in herpes simplex virus as a potential host factor.
- 10

Sample sbg563917RDP	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Avera ge GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	35.34, 40	3.66	0	1.83	3.06	16.34	29.90
Subcutaneous Adipose Zenbio	40, 40	0		0.00	0.96	52.36	0.00
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	30.09, 30.01	91.85	96.8	94.33	7.24	6.91	651.42
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	35.19, 40	4.03	0	2.02	2.17	23.04	46.43
Cervix	36.08, 40	2.33	0	1.17	2.42	20.66	24.07
Colon	36.07, 35.1	2.35	4.24	3.30	2.71	18.45	60.79
Endometrium	35.01, 40	4.49	0	2.25	0.73	68.21	153.14
Esophagus	34.94, 40	4.68	0	2.34	1.37	36.50	85.40
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	35.24, 40	3.89	0	1.95	2.58	19.38	37.69
Jejunum	35.37, 33.35	3.6	12.44	8.02	6.60	7.58	60.76
Kidney	40, 34.97	0	4.6	2.30	2.12	23.58	54.25
Liver	33.51, 34.6	11.25	5.78	8.52	1.50	33.33	283.83
Fetal Liver Clontech	33.19, 35.54	13.75	3.25	8.50	10.40	4.81	40.87
Lung	34.32	6.84	2.28	4.56	2.57	19.46	88.72
Mammary Gland Clontech	40, 35.14	0	4.15	2.08	13.00	3.85	7.98

Myometrium	40, 40	0	0.09	0.05	2.34	21.37	0.96
Omentum	36.17, 33.01	2.2	15.32	8.76	3.94	12.69	111.17
Ovary	40, 40	0	0	0.00	4.34	11.52	0.00
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	35.43, 39.81	3.46	0.24	1.85	5.48	9.12	16.88
Placenta Clontech	33.7, 35.45	10.02	3.42	6.72	5.26	9.51	63.88
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 40	0	0	0.00	1.23	40.65	0.00
Salivary Gland Clontech	34.89, 40	4.83	0	2.42	7.31	6.84	16.52
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	35.01, 33.36	4.48	12.38	8.43	4.92	10.16	85.67
Stomach	33.38, 34.18	12.18	7.48	9.83	2.73	18.32	180.04
Testis Clontech	34.25, 32.86	7.17	16.84	12.01	0.57	87.87	1054.92
Thymus Clontech	32.14, 33.25	26.17	13.24	19.71	9.89	5.06	99.62
Thyroid	40, 40	0	0.09	0.05	2.77	18.05	0.81
Trachea Clontech	31.41, 31	41.04	52.65	46.85	9.71	5.15	241.22
Urinary Bladder	40, 35.05	0	4.38	2.19	5.47	9.14	20.02
Uterus	33.77, 33.41	9.62	12	10.81	5.34	9.36	101.22
genomic	26.54	813.56					
b-actin	27.39	481.34					
1.00E+05	18.71	100000					
1.00E+05	18.92	100000					
1.00E+04	22.44	10000					
1.00E+04	22.11	10000					
1.00E+03	26.05	1000					
1.00E+03	26.11	1000					
1.00E+02	30.4	100					
1.00E+02	30.17	100					
1.00E+01	33.87	10					
1.00E+01	33.26	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg563917RDP	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detecte d/50 ng total RNA	Sample	Fold Change in Disease Population
colon normal GW98-167	21941	30.39	148.35	296.70	colon normal	

colon tumor GW98-166	21940	30.93	110.14	220.28	colon tumor	-1.35
colon normal GW98-178	22080	32.93	36.71	73.42	colon normal	
colon tumor GW98-177	22060	34.8	13.09	26.18	colon tumor	-2.80
colon normal GW98-561	23514	31.41	84.68	169.36	colon normal	
colon tumor GW98-560	23513	32.09	58.33	116.66	colon tumor	-1.45
colon normal GW98-894	24691	30.02	182.15	364.30	colon normal	
colon tumor GW98-893	24690	31.12	99.26	198.52	colon tumor	-1.84
lung normal GW98-3	20742	28.4	443.99	887.98	lung normal	
lung tumor GW98-2	20741	33.59	25.44	50.88	lung tumor	-17.45
lung normal GW97-179	20677	28.63	391.85	783.70	lung normal	
lung tumor GW97-178	20676	29.16	292.08	584.16	lung tumor	-1.34
lung normal GW98-165	21922	29.13	296.8	593.60	lung normal	
lung tumor GW98-164	21921	30.22	163.43	326.86	lung tumor	-1.82
lung normal GW98-282	22584	31.71	71.72	143.44	lung normal	
lung tumor GW98-281	22583	31.74	70.77	141.54	lung tumor	-1.01
breast normal GW00-392	28750	31.49	81.02	81.02	breast normal	
breast tumor GW00-391	28746	33.58	25.62	51.24	breast tumor	-1.58
breast normal GW00-413	28798	35.07	11.31	11.31	breast normal	
breast tumor GW00-412	28797	31.99	61.52	123.04	breast tumor	10.88
breast normal GW00-235:238	27592-95	35.63	8.3	8.30	breast normal	
breast tumor GW00-231:234	27588-91	34.33	16.97	16.97	breast tumor	2.04
breast normal GW98-621	23656	32.07	58.95	117.90	breast normal	
breast tumor GW98-620	23655	32.71	41.33	82.66	breast tumor	-1.43
brain normal BB99-542	25507	30.16	168.86	337.72	brain normal	
brain normal BB99-406	25509	31.12	99.35	198.70	brain normal	
brain normal BB99-904	25546	31.14	98.44	196.88	brain normal	
brain stage 5 ALZ BB99-874	25502	33.16	32.39	64.78	brain stage 5 ALZ	-3.77
brain stage 5 ALZ BB99-887	25503	29.32	267.28	534.56	brain stage 5 ALZ	2.19
brain stage 5 ALZ BB99-862	25504	30.36	150.72	301.44	brain stage 5 ALZ	1.23
brain stage 5 ALZ BB99-927	25542	30.1	174.01	348.02	brain stage 5 ALZ	1.42
CT lung KC	normal	31.06	102.88	205.76	CT lung	
lung 26 KC	normal	32.15	56.21	56.21	lung 26	
lung 27 KC	normal	35.96	6.92	6.92	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-70.34
lung 28 KC	COPD	36.21	6.05	6.05	lung 28	-11.63
lung 23 KC	COPD	34.83	12.87	12.87	lung 23	-5.47
lung 25 KC	normal	34.89	12.45	12.45	lung 25	
asthmatic lung ODO3112	29321	32.57	44.76	44.76	asthmatic lung	-1.57
asthmatic lung ODO3433	29323	32.4	49.04	98.08	asthmatic lung	1.39
asthmatic lung ODO3397	29322	31.79	68.64	137.28	asthmatic lung	1.95
asthmatic lung ODO4928	29325	31.34	88.11	176.22	asthmatic lung	2.51
endo cells KC	control	35.77	7.68	7.68	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	-7.68

endo bFGF KC		40	0	0.00	endo bFGF	-7.68
heart Clontech	normal	31.09	100.75	201.50	heart	
heart (T-1) ischemic	29417	34.75	13.46	26.92	heart T-1	-7.49
heart (T-14) non-obstructive DCM	29422	33.69	24.17	48.34	heart T-14	-4.17
heart (T-3399) DCM	29426	33.48	27.16	54.32	heart T-3399	-3.71
adenoid GW99-269	26162	30.49	140.7	281.40	adenoid	
tonsil GW98-280	22582	30.07	177.32	354.64	tonsil	
T cells PC00314	28453	27.79	622.1	1244.20	T cells	
PBMNC		36.19	6.11	6.11	PBMNC	
monocyte		33.24	30.91	61.82	monocyte	
B cells PC00665	28455	26.37	1355.2	2710.40	B cells	
dendritic cells 28441		28.69	378.62	757.24	dendritic cells	
neutrophils	28440	23.28	7420.47	7420.47	neutrophils	
eosinophils	28446	25.33	2408.94	4817.88	eosinophils	
BM unstim		32.24	53.57	53.57	BM unstim	
BM stim		31.92	64.05	64.05	BM stim	1.20
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		37.59	2.82	7.05	chondrocytes	
OA Synovium IP12/01	29462	31.77	69.48	69.48	OA Synovium	
OA Synovium NP10/01	29461	31.16	96.93	193.86	OA Synovium	
OA Synovium NP57/00	28464	30.84	115.69	231.38	OA Synovium	
RA Synovium NP03/01	28466	30.96	108.37	216.74	RA Synovium	
RA Synovium NP71/00	28467	29.2	285.91	571.82	RA Synovium	
RA Synovium NP45/00	28475	29.87	198.12	396.24	RA Synovium	
OA bone (biobank)	29217	29.67	220.64	220.64	OA bone (biobank)	
OA bone Sample 1	J. Emory	30.54	136.41	272.82	OA bone	
OA bone Sample 2	J. Emory	29.38	259.07	518.14	OA bone	
Cartilage (pool)	Normal	31.34	87.88	175.76	Cartilage (pool)	
Cartilage (pool)	OA	32.9	37.23	74.46	Cartilage (pool)	-2.36
PBL uninfected	28441	30.55	135.85	271.70	PBL uninfected	
PBL HIV IIIB	28442	31.02	104.8	209.60	PBL HIV IIIB	-1.30
MRC5 uninfected (100%)	29158	35.11	11.06	22.12	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	29.63	226.14	452.28	MRC5 HSV strain F	20.45
W12 cells	29179	37.87	2.42	4.84	W12 cells	
Keratinocytes	29180	36.14	6.26	12.52	Keratinocytes	
B-actin control		27.14	887.42			
genomic		26.16	1520.17			
1.00E+05		19.22	100000			
1.00E+05		19.2	100000			
1.00E+04		22.49	10000			
1.00E+04		22.62	10000			
1.00E+03		26.23	1000			
1.00E+03		26.05	1000			
1.00E+02		30.26	100			

1.00E+02		31.03	100			
1.00E+01		38.68	10			
1.00E+01		33.47	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg563917RDP

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.35
colon tumor	-2.80
colon tumor	-1.45
colon tumor	-1.84
lung tumor	-17.45
lung tumor	-1.34
lung tumor	-1.82
lung tumor	-1.01
breast tumor	-1.58
breast tumor	10.88
breast tumor	2.04
breast tumor	-1.43
brain stage 5 ALZ	-3.77
brain stage 5 ALZ	2.19
brain stage 5 ALZ	1.23
brain stage 5 ALZ	1.42
lung 24	-70.34
lung 28	-11.63
lung 23	-5.47
asthmatic lung	-1.57
asthmatic lung	1.39
asthmatic lung	1.95
asthmatic lung	2.51
endo VEGF	-7.68
endo bFGF	-7.68
heart T-1	-7.49
heart T-14	-4.17
heart T-3399	-3.71
BM stim	1.20
osteo undif	0.00
Cartilage (pool)	-2.36
PBL HIV IIIB	-1.30
MRC5 HSV strain F	20.45

5 Gene Name sbg618069LRR

Low overall expression in normal and disease samples. Highest normal expression in whole brain, fetal brain, cerebellum, and thymus. Highest disease expression in one of the colon tumor samples, one of the lung tumor samples, and the uninfected PBL cells. Downregulation in 2 of 4 colon tumors suggests a role in cancer of the colon. Upregulation in 1 of 4 lung tumors and upregulation in 2 of 4 breast tumors suggest roles in cancers of the lung and breast. Downregulation in 3 of 3 COPD lung samples implicates a role for this gene in COPD. Upregulation in the stimulated bone marrow. Downregulation in an HIV-infected cell line as well as moderate expression in immune

cells suggests an involvement in HIV. Upregulation in HSV implicates involvement in herpes simplex virus as a potential host factor.

Sample sbg618069LRR	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	35.24, 34.33	4.38	7.65	6.02	3.06	16.34	98.28
Subcutaneous Adipose Zenbio	40, 40	0	0.08	0.04	0.96	52.36	2.09
Adrenal Gland Clontech	39.9, 38.74	0.13	0.51	0.32	0.61	81.97	26.23
Whole Brain Clontech	27.02, 26.51	673.36	916.93	795.15	7.24	6.91	5491.33
Fetal Brain Clontech	40, 40	0.13	6.01	3.07	0.48	103.95	319.13
Cerebellum Clontech	32.15, 32.13	28.98	29.44	29.21	2.17	23.04	673.04
Cervix	40, 40	0	0	0.00	2.42	20.66	0.00
Colon	36.53, 39.88	1.98	0.25	1.12	2.71	18.45	20.57
Endometrium	37.98, 40	0.82	0.19	0.51	0.73	68.21	34.45
Esophagus	38.86, 40	0.48	0.15	0.32	1.37	36.50	11.50
Heart Clontech	34.17, 34.72	8.41	6.03	7.22	1.32	37.88	273.48
Hypothalamus	40, 40	0	0.07	0.04	0.32	155.28	5.43
Ileum	40, 40	0.17	0.11	0.14	2.58	19.38	2.71
Jejunum	33.07, 34.34	16.52	7.58	12.05	6.60	7.58	91.29
Kidney	36.05, 40	2.67	0.21	1.44	2.12	23.58	33.96
Liver	38.72, 40	0.52	0.61	0.57	1.50	33.33	18.83
Fetal Liver Clontech	33.28, 36.35	14.52	2.22	8.37	10.40	4.81	40.24
Lung	40, 40	0.13	0.08	0.11	2.57	19.46	2.04
Mammary Gland Clontech	40, 34.19	0	8.33	4.17	13.00	3.85	16.02
Myometrium	40, 40	0.28	0	0.14	2.34	21.37	2.99
Omentum	35.01, 35.36	5.04	4.07	4.56	3.94	12.69	57.80
Ovary	34.24, 40	8.07	0.26	4.17	4.34	11.52	47.98
Pancreas	40, 40	0.11	0.13	0.12	0.81	61.80	7.42
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	34.01, 34.28	9.31	7.9	8.61	5.48	9.12	78.51
Placenta Clontech	40, 40	0	0.07	0.04	5.26	9.51	0.33
Prostate	40, 39.13	0.15	0.4	0.28	3.00	16.67	4.58
Rectum	40, 39.55	0.21	0.31	0.26	1.23	40.65	10.57
Salivary Gland Clontech	32.35, 33.08	25.74	16.45	21.10	7.31	6.84	144.29
Skeletal Muscle Clontech	34.78, 40	5.81	0.27	3.04	1.26	39.68	120.63
Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	40, 40	0.16	0	0.08	0.98	51.07	4.09
Spleen	35.59, 40	3.53	0.59	2.06	4.92	10.16	20.93
Stomach	36.73, 40	1.76	0.11	0.94	2.73	18.32	17.12
Testis Clontech	37.91, 40	0.86	0.1	0.48	0.57	87.87	42.18

Thymus Clontech	30.22, 29.94	94.88	112.23	103.56	9.89	5.06	523.53
Thyroid	35.15, 40	4.62	0	2.31	2.77	18.05	41.70
Trachea Clontech	33.49, 34.21	12.75	8.22	10.49	9.71	5.15	53.99
Urinary Bladder	40, 40	0.09	0.08	0.09	5.47	9.14	0.78
Uterus	35.26, 33.03	4.31	16.97	10.64	5.34	9.36	99.63
genomic	26.04	1229.54					
b-actin	27.25	584.19					
1.00E+05	19.09	100000					
1.00E+05	19.04	100000					
1.00E+04	22.35	10000					
1.00E+04	22.35	10000					
1.00E+03	26.07	1000					
1.00E+03	26.26	1000					
1.00E+02	30.64	100					
1.00E+02	30.38	100					
1.00E+01	34.04	10					
1.00E+01	33.52	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg618069LRR	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detecte d/50 ng total RNA	Sample	Fold Change in Disease Populati on
colon normal GW98-167	21941	29.52	176.51	353.02	colon normal	
colon tumor GW98-166	21940	33.45	18.5	37.00	colon tumor	-9.54
colon normal GW98-178	22080	31.82	47.14	94.28	colon normal	
colon tumor GW98-177	22060	29.68	160.67	321.34	colon tumor	3.41
colon normal GW98-561	23514	30.33	110.78	221.56	colon normal	
colon tumor GW98-560	23513	33.11	22.39	44.78	colon tumor	-4.95
colon normal GW98-894	24691	28.1	396.95	793.90	colon normal	
colon tumor GW98-893	24690	26.93	779.99	1559.98	colon tumor	1.96
lung normal GW98-3	20742	30.41	105.78	211.56	lung normal	
lung tumor GW98-2	20741	26.28	1128.28	2256.56	lung tumor	10.67
lung normal GW97-179	20677	29.28	201.91	403.82	lung normal	
lung tumor GW97-178	20676	28.35	345.36	690.72	lung tumor	1.71
lung normal GW98-165	21922	28.42	331.95	663.90	lung normal	
lung tumor GW98-164	21921	30.98	76.05	152.10	lung tumor	-4.36
lung normal GW98-282	22584	34.15	12.36	24.72	lung normal	
lung tumor GW98-281	22583	32.08	40.6	81.20	lung tumor	3.28
breast normal GW00-392	28750	29.67	161.68	161.68	breast normal	
breast tumor GW00-391	28746	28.98	239.65	479.30	breast tumor	2.96
breast normal GW00-413	28798	31.78	48.04	48.04	breast normal	

breast tumor GW00-412	28797	29.69	159.55	319.10	breast tumor	6.64
breast normal GW00-235:238	27592-95	34.18	12.14	12.14	breast normal	
breast tumor GW00-231:234	27588-91	29.2	211.28	211.28	breast tumor	17.40
breast normal GW98-621	23656	29.72	157.4	314.80	breast normal	
breast tumor GW98-620	23655	31.12	70.17	140.34	breast tumor	-2.24
brain normal BB99-542	25507	30.81	83.89	167.78	brain normal	
brain normal BB99-406	25509	31.02	74.28	148.56	brain normal	
brain normal BB99-904	25546	31.39	60.08	120.16	brain normal	
brain stage 5 ALZ BB99-874	25502	32.54	31.07	62.14	brain stage 5 ALZ	-2.34
brain stage 5 ALZ BB99-887	25503	30.65	92.1	184.20	brain stage 5 ALZ	1.27
brain stage 5 ALZ BB99-862	25504	31.68	50.92	101.84	brain stage 5 ALZ	-1.43
brain stage 5 ALZ BB99-927	25542	31.39	60.36	120.72	brain stage 5 ALZ	-1.21
CT lung KC	normal	30.47	101.87	203.74	CT lung	
lung 26 KC	normal				lung 26	
lung 27 KC	normal	39.27	0.65	0.65	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-68.13
lung 28 KC	COPD	37.38	1.93	1.93	lung 28	-35.30
lung 23 KC	COPD	34.28	11.47	11.47	lung 23	-5.94
lung 25 KC	normal	40	0	0.00	lung 25	
asthmatic lung ODO3112	29321	33.17	21.73	21.73	asthmatic lung	-3.14
asthmatic lung ODO3433	29323	32.35	34.64	69.28	asthmatic lung	1.02
asthmatic lung ODO3397	29322	30.83	83.1	166.20	asthmatic lung	2.44
asthmatic lung ODO4928	29325	30.94	77.99	155.98	asthmatic lung	2.29
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		40	0	0.00	endo bFGF	0.00
heart Clontech	normal	30.52	99.45	198.90	heart	
heart (T-1) ischemic	29417	28.78	270.18	540.36	heart T-1	2.72
heart (T-14) non-obstructive DCM	29422	29.62	166.76	333.52	heart T-14	1.68
heart (T-3399) DCM	29426	30.05	129.76	259.52	heart T-3399	1.30
adenoid GW99-269	26162	29.05	230.93	461.86	adenoid	
tonsil GW98-280	22582	29.77	152.22	304.44	tonsil	
T cells PC00314	28453	31.6	53.48	106.96	T cells	
PBMNC		39.8	0.48	0.48	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	31.56	54.77	109.54	B cells	
dendritic cells 28441		34.09	12.8	25.60	dendritic cells	
neutrophils	28440	34.03	13.21	13.21	neutrophils	
eosinophils	28446	40	0	0.00	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim		35.71	5.04	5.04	BM stim	5.04
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	

chondrocytes		33.5	17.89	44.73	chondrocytes	
OA Synovium IP12/01	29462	32.24	37.02	37.02	OA Synovium	
OA Synovium NP10/01	29461	27.95	434.95	869.90	OA Synovium	
OA Synovium NP57/00	28464	30.9	79.82	159.64	OA Synovium	
RA Synovium NP03/01	28466	31.79	47.9	95.80	RA Synovium	
RA Synovium NP71/00	28467	33.06	23.05	46.10	RA Synovium	
RA Synovium NP45/00	28475	32.76	27.41	54.82	RA Synovium	
OA bone (biobank)	29217	32.02	42.02	42.02	OA bone (biobank)	
OA bone Sample 1	J. Emory	31.32	62.63	125.26	OA bone	
OA bone Sample 2	J. Emory	33.13	22.24	44.48	OA bone	
Cartilage (pool)	Normal	30.76	86.51	173.02	Cartilage (pool)	
Cartilage (pool)	OA	33.13	22.15	44.30	Cartilage (pool)	-3.91
PBL uninfected	28441	26.78	847.01	1694.02	PBL uninfected	
PBL HIV IIIB	28442	28.21	374.26	748.52	PBL HIV IIIB	-2.26
MRC5 uninfected (100%)	29158	40	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	31.26	64.96	129.92	MRC5 HSV strain F	129.92
W12 cells	29179	40	0	0.00	W12 cells	
Keratinocytes	29180	39.77	0.49	0.98	Keratinocytes	
B-actin control		27.18	675.17			
genomic		25.96	1358.6			
1.00E+05		18.58	100000			
1.00E+05		18.53	100000			
1.00E+04		22.04	10000			
1.00E+04		22.1	10000			
1.00E+03		25.85	1000			
1.00E+03		26.11	1000			
1.00E+02		34.02	100			
1.00E+02		30.53	100			
1.00E+01		32.98	10			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		38.21	1			
NTC		40	0			

Gene Name sbg618069LRR

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-9.54
colon tumor	3.41
colon tumor	-4.95
colon tumor	1.96
lung tumor	10.67
lung tumor	1.71
lung tumor	-4.36
lung tumor	3.28

breast tumor	2.96
breast tumor	6.64
breast tumor	17.40
breast tumor	-2.24
brain stage 5 ALZ	-2.34
brain stage 5 ALZ	1.27
brain stage 5 ALZ	-1.43
brain stage 5 ALZ	-1.21
lung 24	-68.13
lung 28	-35.30
lung 23	-5.94
asthmatic lung	-3.14
asthmatic lung	1.02
asthmatic lung	2.44
asthmatic lung	2.29
endo VEGF	0.00
endo bFGF	0.00
heart T-1	2.72
heart T-14	1.68
heart T-3399	1.30
BM stim	5.04
osteo dif	0.00
Cartilage (pool)	-3.91
PBL HIV IIIB	-2.26
MRC5 HSV strain F	129.92

Gene Name sbg934114Relaxin

- 5 Low overall expression in normal and disease samples. Highest normal expression in testis, liver, and whole brain. Highest disease expression in 3 of the normal lung samples, one of the normal tumor samples, the HSV-infected MRC5 cells, the adenoid, and the T cells. Highest disease
- 10 expression in 2 of the normal lung samples, one of the lung tumor samples, 1 of the normal breast samples, 1 of the breast tumor samples, and the uninfected PBL samples. Downregulation in 1 of 4 colon tumors and downregulation in 2 of 4 lung tumors imply roles in cancers of the colon and lung.
- 15 Downregulation in 3 of 3 COPD lung samples and upregulation in 3 of 4 asthmatic lung samples implicates this gene in COPD and asthma. Upregulation in 2 of 3 heart samples proposes roles in non-obstructive and obstructive DCM. Downregulation in the OA cartilage pool and low expression in RA and OA synovium, OA bone, and chondrocytes suggests an involvement in osteoarthritis and rheumatoid arthritis. Downregulation in an HIV-infected primary cell line suggests an involvement in HIV. Upregulation in HSV implicates involvement in herpes simplex virus as a potential host factor.

Sample sbg934114Relaxin	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	37.4, 40	5.41	0	2.71	3.06	16.34	44.20

Subcutaneous Adipose Zenbio	40, 40	0.73	0	0.37	0.96	52.36	19.11
Adrenal Gland Clontech	40, 40	0.73	0.69	0.71	0.61	81.97	58.20
Whole Brain Clontech	33.52, 34.72	47.76	24.26	36.01	7.24	6.91	248.69
Fetal Brain Clontech	39.51, 40	1.65	0.86	1.26	0.48	103.95	130.46
Cerebellum Clontech	40, 39.84	0.99	1.37	1.18	2.17	23.04	27.19
Cervix	40, 40	1.05	0	0.53	2.42	20.66	10.85
Colon	40, 37.31	0	5.7	2.85	2.71	18.45	52.58
Endometrium	40, 40	0	0	0.00	0.73	68.21	0.00
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	38.11, 40	3.63	1.31	2.47	1.32	37.88	93.56
Hypothalamus	40, 40	0	1.06	0.53	0.32	155.28	82.30
Ileum	40, 36.79	0	7.62	3.81	2.58	19.38	73.84
Jejunum	35.14, 35.9	19.25	12.54	15.90	6.60	7.58	120.42
Kidney	40, 40	0	0	0.00	2.12	23.58	0.00
Liver	37.25, 35.17	5.88	18.92	12.40	1.50	33.33	413.33
Fetal Liver Clontech	40, 37.38	0.73	5.47	3.10	10.40	4.81	14.90
Lung	37.07, 40	6.52	0	3.26	2.57	19.46	63.42
Mammary Gland Clontech	40, 40	0	0	0.00	13.00	3.85	0.00
Myometrium	37.95, 40	3.98	0	1.99	2.34	21.37	42.52
Omentum	36.24, 37.04	10.39	6.63	8.51	3.94	12.69	107.99
Ovary	35.29, 36.26	17.66	10.28	13.97	4.34	11.52	160.94
Pancreas	39.48, 40	1.69	0	0.85	0.81	61.80	52.22
Head of Pancreas	36.17, 39.82	10.79	1.39	6.09	1.57	31.85	193.95
Parotid Gland	40, 38.66	0	2.67	1.34	5.48	9.12	12.18
Placenta Clontech	40, 36.57	0	8.63	4.32	5.26	9.51	41.02
Prostate	36.91, 40	7.14	0	3.57	3.00	16.67	59.50
Rectum	40, 37.34	0	5.61	2.81	1.23	40.65	114.02
Salivary Gland Clontech	40, 40	0	0	0.00	7.31	6.84	0.00
Skeletal Muscle Clontech	40, 39.45	0	1.71	0.86	1.26	39.68	33.93
Skin	39.2, 40	1.98	0	0.99	1.21	41.32	40.91
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	36, 40	11.84	0	5.92	4.92	10.16	60.16
Stomach	35.48, 39.19	15.9	1.98	8.94	2.73	18.32	163.74
Testis Clontech	40, 36.09	0	11.27	5.64	0.57	87.87	495.17
Thymus Clontech	34.34, 36.66	30.03	8.2	19.12	9.89	5.06	96.64
Thyroid	40, 40	0	0	0.00	2.77	18.05	0.00
Trachea Clontech	40, 37.8	0	4.33	2.17	9.71	5.15	11.15
Urinary Bladder	40, 40	0	0	0.00	5.47	9.14	0.00
Uterus	37.11, 35.16	6.36	18.96	12.66	5.34	9.36	118.54
genomic	27.61	1307.98					
b-actin	27.15	1697.68					
1.00E+05	19.88	100000					
1.00E+05	20.05	100000					
1.00E+04	24.01	10000					

1.00E+04	23.92	10000					
1.00E+03	27.98	1000					
1.00E+03	27.6	1000					
1.00E+02	32.89	100					
1.00E+02	32.2	100					
1.00E+01	36.1	10					
1.00E+01							
1.00E-00							
1.00E-00							
NTC	40	0					
NTC	40	0					

Sample sbg934114Relaxin	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detecte d/50 ng total RNA	Sample	Fold Change in Disease Populati on
colon normal GW98-167	21941	36.1	22.33	44.66	colon normal	
colon tumor GW98-166	21940	36.47	18.37	36.74	colon tumor	-1.22
colon normal GW98-178	22080	35.7	27.58	55.16	colon normal	
colon tumor GW98-177	22060	38.05	7.98	15.96	colon tumor	-3.46
colon normal GW98-561	23514	33.57	84.85	169.70	colon normal	
colon tumor GW98-560	23513	37.66	9.8	19.60	colon tumor	-8.66
colon normal GW98-894	24691	36.39	19.09	38.18	colon normal	
colon tumor GW98-893	24690	36.43	18.74	37.48	colon tumor	-1.02
lung normal GW98-3	20742	32.48	150.6	301.20	lung normal	
lung tumor GW98-2	20741	36.65	16.64	33.28	lung tumor	-9.05
lung normal GW97-179	20677	33.22	102.07	204.14	lung normal	
lung tumor GW97-178	20676	32.31	164.63	329.26	lung tumor	1.61
lung normal GW98-165	21922	32.08	185.96	371.92	lung normal	
lung tumor GW98-164	21921	35.14	37.09	74.18	lung tumor	-5.01
lung normal GW98-282	22584	36.41	18.93	37.86	lung normal	
lung tumor GW98-281	22583	35.24	35.13	70.26	lung tumor	1.86
breast normal GW00-392	28750	34.04	66.25	66.25	breast normal	
breast tumor GW00-391	28746	37.9	8.61	17.22	breast tumor	-3.85
breast normal GW00-413	28798	36.36	19.44	19.44	breast normal	
breast tumor GW00-412	28797	36.79	15.49	30.98	breast tumor	1.59
breast normal GW00-235:238	27592-95	36.91	14.52	14.52	breast normal	
breast tumor GW00-231:234	27588-91	35.43	31.71	31.71	breast tumor	2.18
breast normal GW98-621	23656	36.26	20.51	41.02	breast normal	
breast tumor GW98-620	23655	35.76	26.68	53.36	breast tumor	1.30
brain normal BB99-542	25507	37.99	8.21	16.42	brain normal	
brain normal BB99-406	25509	40	1.41	2.82	brain normal	
brain normal BB99-904	25546	40	0	0.00	brain normal	
brain stage 5 ALZ BB99-	25502	38.65	5.82	11.64	brain stage 5 ALZ	1.81

874						
brain stage 5 ALZ BB99-887	25503	37	13.9	27.80	brain stage 5 ALZ	4.33
brain stage 5 ALZ BB99-862	25504	37.4	11.24	22.48	brain stage 5 ALZ	3.51
brain stage 5 ALZ BB99-927	25542	38	8.19	16.38	brain stage 5 ALZ	2.55
CT lung KC	normal	35.32	33.59	67.18	CT lung	
lung 26 KC	normal	37.02	13.72	13.72	lung 26	
lung 27 KC	normal	40	0	0.00	lung 27	
lung 24 KC	COPD	39.97	2.78	2.78	lung 24	-7.81
lung 28 KC	COPD	40	0	0.00	lung 28	-21.71
lung 23 KC	COPD	39.06	4.67	4.67	lung 23	-4.65
lung 25 KC	normal	38.61	5.92	5.92	lung 25	
asthmatic lung ODO3112	29321	36.02	23.31	23.31	asthmatic lung	1.07
asthmatic lung ODO3433	29323	34.12	63.36	126.72	asthmatic lung	5.84
asthmatic lung ODO3397	29322	33.99	68.06	136.12	asthmatic lung	6.27
asthmatic lung ODO4928	29325	33.77	76.08	152.16	asthmatic lung	7.01
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		38.16	7.54	7.54	endo bFGF	7.54
heart Clontech	normal	40	0	0.00	heart	
heart (T-1) ischemic	29417	40	1.36	2.72	heart T-1	2.72
heart (T-14) non-obstructive DCM	29422	36.31	20.01	40.02	heart T-14	40.02
heart (T-3399) DCM	29426	37.17	12.7	25.40	heart T-3399	25.40
adenoid GW99-269	26162	33.33	96.07	192.14	adenoid	
tonsil GW98-280	22582	34.86	42.85	85.70	tonsil	
T cells PC00314	28453	33.48	88.65	177.30	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	32.44	153.68	307.36	B cells	
dendritic cells 28441		35.78	26.47	52.94	dendritic cells	
neutrophils	28440	36.18	21.43	21.43	neutrophils	
eosinophils	28446	39.2	4.34	8.68	eosinophils	
BM unstim		39.56	3.6	3.60	BM unstim	
BM stim		40	1.34	1.34	BM stim	-2.69
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		36.64	16.79	41.98	chondrocytes	
OA Synovium IP12/01	29462	34.75	45.45	45.45	OA Synovium	
OA Synovium NP10/01	29461	36.02	23.28	46.56	OA Synovium	
OA Synovium NP57/00	28464	34.24	59.37	118.74	OA Synovium	
RA Synovium NP03/01	28466	37.88	8.71	17.42	RA Synovium	
RA Synovium NP71/00	28467	36.02	23.22	46.44	RA Synovium	
RA Synovium NP45/00	28475	34.9	41.9	83.80	RA Synovium	
OA bone (biobank)	29217	33.59	83.75	83.75	OA bone (biobank)	
OA bone Sample 1	J. Emory	37.31	11.8	23.60	OA bone	

OA bone Sample 2	J. Emory	37.47	10.81	21.62	OA bone	
Cartilage (pool)	Normal	34.61	49.07	98.14	Cartilage (pool)	
Cartilage (pool)	OA	40	0	0.00	Cartilage (pool)	-98.14
PBL uninfected	28441	33.86	72.8	145.60	PBL uninfected	
PBL HIV IIIB	28442	37.08	13.28	26.56	PBL HIV IIIB	-5.48
MRC5 uninfected (100%)	29158	39.01	4.81	9.62	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	31.5	252.68	505.36	MRC5 HSV strain F	52.53
W12 cells	29179	39.84	3.1	6.20	W12 cells	
Keratinocytes	29180	39.07	4.64	9.28	Keratinocytes	
B-actin control		27.9	1683.49			
genomic		28.13	1492.71			
1.00E+05		20.5	100000			
1.00E+05		20.61	100000			
1.00E+04		24.56	10000			
1.00E+04		24.17	10000			
1.00E+03		28.14	1000			
1.00E+03		28.32	1000			
1.00E+02		34.26	100			
1.00E+02		32.76	100			
1.00E+01		38.07	10			
1.00E+01		37.53	10			
1.00E-00		40	0			
1.00E-00		40	1			
NTC		38.42	-1			

Gene Name sbg934114Relaxin

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.22
colon tumor	-3.46
colon tumor	-8.66
colon tumor	-1.02
lung tumor	-9.05
lung tumor	1.61
lung tumor	-5.01
lung tumor	1.86
breast tumor	-3.85
breast tumor	1.59
breast tumor	2.18
breast tumor	1.30
brain stage 5 ALZ	1.81
brain stage 5 ALZ	4.33
brain stage 5 ALZ	3.51
brain stage 5 ALZ	2.55
lung 24	-7.81
lung 28	-21.71
lung 23	-4.65
asthmatic lung	1.07

asthmatic lung	5.84
asthmatic lung	6.27
asthmatic lung	7.01
endo VEGF	0.00
endo bFGF	7.54
heart T-1	2.72
heart T-14	40.02
heart T-3399	25.40
BM stim	-2.69
osteo dif	0.00
Cartilage (pool)	-98.14
PBL HIV IIIB	-5.48
MRC5 HSV strain F	52.53

Gene Name sbg99174LOX-like

5 Moderate overall expression in normal and disease samples. Highest normal expression in whole brain, liver, skin, spleen, testis. Shows relatively good expression in the female reproductive samples as well as the GI tract samples. Highest disease expression in one of the normal lung samples, one of the asthmatic lung samples, neutrophils, eosinophils, 2 of the RA synovium samples, and one of the OA bone samples. Downregulation in 1 of 4 lung tumor samples suggests possible implication in lung cancer. Upregulation in 2 of 4 breast tumors implies an involvement in

10 cancers of the breast. Downregulation in 1 of 4 AD brains along with the high expression seen in the brain suggests an involvement in Alzheimer's disease. Downregulation in 2 of 3 COPD lung samples implies an involvement in chronic obstructive pulmonary disease. Upregulation in 1 of 4 asthmatic lung samples implies a role in asthma. Downregulation in OA cartilage and high

15 expression in OA and RA synovium suggests possible involvement in osteoarthritis and rheumatoid arthritis. Corroborating high expression in the T cells provides additional evidence for a role in RA/OA. Moderate expression in other immune cells.

Sample sbg99174LOX-like	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	39.67, 34.48	0.53	11.91	6.22	3.06	16.34	101.63
Subcutaneous Adipose Zenbio	40, 39.75	0.39	0.51	0.45	0.96	52.36	23.56
Adrenal Gland Clontech	38.61, 37.69	1	1.75	1.38	0.61	81.97	112.70
Whole Brain Clontech	30.59, 31.07	122.95	92.57	107.76	7.24	6.91	744.20
Fetal Brain Clontech	40, 40	0	0.29	0.15	0.48	103.95	15.07
Cerebellum Clontech	40, 40	0.4	0.4	0.40	2.17	23.04	9.22
Cervix	35.77, 40	5.52	0.62	3.07	2.42	20.66	63.43
Colon	40, 39.41	0.34	0.62	0.48	2.71	18.45	8.86
Endometrium	40, 38.65	0	0.98	0.49	0.73	68.21	33.42
Esophagus	40, 40	0.35	0.41	0.38	1.37	36.50	13.87
Heart Clontech	39.33, 40	0.65	0	0.33	1.32	37.88	12.31
Hypothalamus	40, 39.54	0	0.58	0.29	0.32	155.28	45.03
Ileum	35.42, 35.76	6.79	5.55	6.17	2.58	19.38	119.57
Jejunum	34.13, 33.4	14.77	22.9	18.84	6.60	7.58	142.69

Kidney	40, 37.22	0.68	2.32	1.50	2.12	23.58	35.38
Liver	33.5, 33.86	21.47	17.3	19.39	1.50	33.33	646.17
Fetal Liver Clontech	32.78, 33.23	33.08	25.33	29.21	10.40	4.81	140.41
Lung	33.96, 34.44	16.33	12.25	14.29	2.57	19.46	278.02
Mammary Gland Clontech	35.05, 36.02	8.51	4.76	6.64	13.00	3.85	25.52
Myometrium	35.08, 35.49	8.34	6.52	7.43	2.34	21.37	158.76
Omentum	37.6, 35.05	1.83	8.49	5.16	3.94	12.69	65.48
Ovary	35.57, 32.76	6.21	33.46	19.84	4.34	11.52	228.51
Pancreas	40, 40	0	0.42	0.21	0.81	61.80	12.98
Head of Pancreas	40, 38.65	0.56	0.98	0.77	1.57	31.85	24.52
Parotid Gland	35.28, 40	7.4	0.64	4.02	5.48	9.12	36.68
Placenta Clontech	40, 39.17	0.32	0.72	0.52	5.26	9.51	4.94
Prostate	40, 35.34	0	7.15	3.58	3.00	16.67	59.58
Rectum	37.29, 39.02	2.22	0.78	1.50	1.23	40.65	60.98
Salivary Gland Clontech	40, 38.15	0.27	1.32	0.80	7.31	6.84	5.44
Skeletal Muscle Clontech	40, 38.56	0.56	1.03	0.80	1.26	39.68	31.55
Skin	35.1, 34.19	8.22	14.22	11.22	1.21	41.32	463.64
Small Intestine Clontech	40, 40	0	0.85	0.43	0.98	51.07	21.71
Spleen	32.2, 32.08	46.76	50.49	48.63	4.92	10.16	494.16
Stomach	34.28, 34.07	13.5	15.3	14.40	2.73	18.32	263.74
Testis Clontech	34.05, 32.7	15.46	34.82	25.14	0.57	87.87	2209.14
Thymus Clontech	33.85, 32.4	17.44	41.71	29.58	9.89	5.06	149.52
Thyroid	34.22, 34.29	13.93	13.37	13.65	2.77	18.05	246.39
Trachea Clontech	32.51, 32.4	38.89	41.53	40.21	9.71	5.15	207.05
Urinary Bladder	35.47, 40	6.6	0	3.30	5.47	9.14	30.16
Uterus	33.8, 33.6	18.01	20.22	19.12	5.34	9.36	178.98
genomic	26.31	1603.29					
b-actin	27.35	860.96					
1.00E+05	19.71	100000					
1.00E+05	19.88	100000					
1.00E+04	22.98	10000					
1.00E+04	23.01	10000					
1.00E+03	26.44	1000					
1.00E+03	26.54	1000					
1.00E+02	31.28	100					
1.00E+02	31.29	100					
1.00E+01	35.79	10					
1.00E+01	34.36	10					
1.00E-00	38.32	1					
1.00E-00	40	1					
NTC	40	0					
NTC	40	0					

Sample sbg99174LOX-like	Reg number	Ct	Mean GOI	copies of	Sample	Fold Change
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	(GSK identifier)		copies	mRNA detecte d/50 ng total RNA		in Disease Populati on
colon normal GW98-167	21941	29.81	184.31	368.62	colon normal	
colon tumor GW98-166	21940	29.25	254.48	508.96	colon tumor	1.38
colon normal GW98-178	22080	32.06	50.31	100.62	colon normal	
colon tumor GW98-177	22060	31.77	59.28	118.56	colon tumor	1.18
colon normal GW98-561	23514	33.21	25.83	51.66	colon normal	
colon tumor GW98-560	23513	31.74	60.51	121.02	colon tumor	2.34
colon normal GW98-894	24691	30.17	149.84	299.68	colon normal	
colon tumor GW98-893	24690	29.41	232.23	464.46	colon tumor	1.55
lung normal GW98-3	20742	25.76	1914.72	3829.44	lung normal	
lung tumor GW98-2	20741	30.12	154.63	309.26	lung tumor	-12.38
lung normal GW97-179	20677	29.59	209.5	419.00	lung normal	
lung tumor GW97-178	20676	27.2	835.04	1670.08	lung tumor	3.99
lung normal GW98-165	21922	28.22	462.22	924.44	lung normal	
lung tumor GW98-164	21921	29.27	251.87	503.74	lung tumor	-1.84
lung normal GW98-282	22584	30.18	149.17	298.34	lung normal	
lung tumor GW98-281	22583	28.47	399.41	798.82	lung tumor	2.68
breast normal GW00-392	28750	30.24	143.58	143.58	breast normal	
breast tumor GW00-391	28746	30.16	151.08	302.16	breast tumor	2.10
breast normal GW00-413	28798	31.51	68.87	68.87	breast normal	
breast tumor GW00-412	28797	28.91	310.66	621.32	breast tumor	9.02
breast normal GW00-235:238	27592-95	40	0	0.00	breast normal	
breast tumor GW00-231:234	27588-91	33.55	21.28	21.28	breast tumor	21.28
breast normal GW98-621	23656	31.57	66.56	133.12	breast normal	
breast tumor GW98-620	23655	31.15	84.8	169.60	breast tumor	1.27
brain normal BB99-542	25507	29.55	214.38	428.76	brain normal	
brain normal BB99-406	25509	29.15	270.89	541.78	brain normal	
brain normal BB99-904	25546	30.48	124.98	249.96	brain normal	
brain stage 5 ALZ BB99-874	25502	33.57	20.99	41.98	brain stage 5 ALZ	-9.69
brain stage 5 ALZ BB99-887	25503	29.89	176.42	352.84	brain stage 5 ALZ	-1.15
brain stage 5 ALZ BB99-862	25504	31.65	63.83	127.66	brain stage 5 ALZ	-3.19
brain stage 5 ALZ BB99-927	25542	31.04	90.73	181.46	brain stage 5 ALZ	-2.24
CT lung KC	normal	29.94	170.8	341.60	CT lung	
lung 26 KC	normal	30.63	115.04	115.04	lung 26	
lung 27 KC	normal	32.22	45.83	45.83	lung 27	
lung 24 KC	COPD	34.16	14.91	14.91	lung 24	-9.21
lung 28 KC	COPD	33.51	21.7	21.70	lung 28	-6.33
lung 23 KC	COPD	32.51	38.67	38.67	lung 23	-3.55
lung 25 KC	normal	32.18	46.79	46.79	lung 25	
asthmatic lung ODO3112	29321	31.84	56.95	56.95	asthmatic lung	-2.41

asthmatic lung ODO3433	29323	31.12	86.42	172.84	asthmatic lung	1.26
asthmatic lung ODO3397	29322	27.13	867.31	1734.62	asthmatic lung	12.63
asthmatic lung ODO4928	29325	30.25	142.92	285.84	asthmatic lung	2.08
endo cells KC	control	31.23	81.05	81.05	endo cells	
endo VEGF KC		31.87	56.15	56.15	endo VEGF	-1.44
endo bFGF KC		32.64	35.97	35.97	endo bFGF	-2.25
heart Clontech	normal	35.46	7.06	14.12	heart	
heart (T-1) ischemic	29417	35.73	6.03	12.06	heart T-1	-1.17
heart (T-14) non-obstructive DCM	29422	34.34	13.49	26.98	heart T-14	1.91
heart (T-3399) DCM	29426	33.65	20.01	40.02	heart T-3399	2.83
adenoid GW99-269	26162	31.2	82.69	165.38	adenoid	
tonsil GW98-280	22582	30.8	103.96	207.92	tonsil	
T cells PC00314	28453	28.16	480.4	960.80	T cells	
PBMNC		30.25	143.11	143.11	PBMNC	
monocyte		30.05	160.68	321.36	monocyte	
B cells PC00665	28455	30.75	107.02	214.04	B cells	
dendritic cells 28441		30.32	137.17	274.34	dendritic cells	
neutrophils	28440	26.32	1390.87	1390.87	neutrophils	
eosinophils	28446	25.07	2854.44	5708.88	eosinophils	
BM unstim		30.72	109.05	109.05	BM unstim	
BM stim		28.61	369.2	369.20	BM stim	3.39
osteo dif		40	0	0.00	osteo dif	-0.28
osteo undif		40	0.28	0.28	osteo undif	
chondrocytes		34.3	13.76	34.40	chondrocytes	
OA Synovium IP12/01	29462	27.56	676.63	676.63	OA Synovium	
OA Synovium NP10/01	29461	31.41	73.19	146.38	OA Synovium	
OA Synovium NP57/00	28464	28.02	518.05	1036.10	OA Synovium	
RA Synovium NP03/01	28466	27.03	921.88	1843.76	RA Synovium	
RA Synovium NP71/00	28467	27.04	914.02	1828.04	RA Synovium	
RA Synovium NP45/00	28475	29.06	285.08	570.16	RA Synovium	
OA bone (biobank)	29217	26.78	1065.84	1065.84	OA bone (biobank)	
OA bone Sample 1	J. Emory	30.27	141.07	282.14	OA bone	
OA bone Sample 2	J. Emory	27.04	917.04	1834.08	OA bone	
Cartilage (pool)	Normal	28.23	461.21	922.42	Cartilage (pool)	
Cartilage (pool)	OA	33.16	26.65	53.30	Cartilage (pool)	-17.31
PBL uninfected	28441	28.72	346.97	693.94	PBL uninfected	
PBL HIV IIIB	28442	28.54	384.02	768.04	PBL HIV IIIB	1.11
MRC5 uninfected (100%)	29158	31.64	64.07	128.14	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	31.53	68.31	136.62	MRC5 HSV strain F	1.07
W12 cells	29179	34.44	12.72	25.44	W12 cells	
Keratinocytes	29180	36.02	5.1	10.20	Keratinocytes	
B-actin control		27.2	835.98			
genomic		26.76	1073.72			
1.00E+05		19.13	100000			
1.00E+05		19.61	100000			

1.00E+04		22.79	10000			
1.00E+04		22.5	10000			
1.00E+03		26.36	1000			
1.00E+03		26.23	1000			
1.00E+02		31.25	100			
1.00E+02		30.82	100			
1.00E+01		35.02	10			
1.00E+01		35.15	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg99174LOX-like

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.38
colon tumor	1.18
colon tumor	2.34
colon tumor	1.55
lung tumor	-12.38
lung tumor	3.99
lung tumor	-1.84
lung tumor	2.68
breast tumor	2.10
breast tumor	9.02
breast tumor	21.28
breast tumor	1.27
brain stage 5 ALZ	-9.69
brain stage 5 ALZ	-1.15
brain stage 5 ALZ	-3.19
brain stage 5 ALZ	-2.24
lung 24	-9.21
lung 28	-6.33
lung 23	-3.55
asthmatic lung	-2.41
asthmatic lung	1.26
asthmatic lung	12.63
asthmatic lung	2.08
endo VEGF	-1.44
endo bFGF	-2.25
heart T-1	-1.17
heart T-14	1.91
heart T-3399	2.83
BM stim	3.39
osteo dif	-0.28
Cartilage (pool)	-17.31
PBL HIV IIIB	1.11
MRC5 HSV strain F	1.07

5 Gene Name sbg995002PIGR (Taqman)

Extremely low overall expression in normal and disease samples. Highest normal expression in the colon and the parotid gland. Highest disease expression in the one of the lung tumors and one of the colon tumors. Upregulation in 1 of 4 colon tumors and 1 of 4 lung tumors imply roles in cancers of the colon and lung. Downregulation in 3 of 4 AD brain samples as well as high expression in whole brain suggests an involvement in Alzheimer's disease. Downregulation in 3 of 3 COPD lung samples implicates this gene in COPD. Downregulation in the ischemic and non-obstructive DCM heart samples suggests a role for this gene in cardiovascular disease. Upregulation in the stimulated bone marrow sample. Upregulation in HSV implicates involvement in herpes simplex virus as a potential host factor. High expression in neutrophils and eosinophils.

Sample sbg995002PIGR	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 40	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	40, 40	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	36.78, 40	11.16	0	5.58	7.24	6.91	38.54
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	40, 40	0	0	0.00	2.17	23.04	0.00
Cervix	40, 40	0	0	0.00	2.42	20.66	0.00
Colon	37.16, 37.12	8.81	9.05	8.93	2.71	18.45	164.76
Endometrium	40, 40	0	0	0.00	0.73	68.21	0.00
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	40, 40	0	0	0.00	2.58	19.38	0.00
Jejunum	40, 40	0	0	0.00	6.60	7.58	0.00
Kidney	40, 40	0	0	0.00	2.12	23.58	0.00
Liver	40, 39.16	0	2.58	1.29	1.50	33.33	43.00
Fetal Liver Clontech	40, 40	0	0	0.00	10.40	4.81	0.00
Lung	40, 40	0	0	0.00	2.57	19.46	0.00
Mammary Gland Clontech	40, 39.18	0	2.55	1.28	13.00	3.85	4.90
Myometrium	40, 40	0	0	0.00	2.34	21.37	0.00
Omentum	40, 38.04	0	5.15	2.58	3.94	12.69	32.68
Ovary	39.29, 40	2.37	0	1.19	4.34	11.52	13.65
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	36.7, 37.94	11.72	5.46	8.59	5.48	9.12	78.38
Placenta Clontech	40, 40	0	0	0.00	5.26	9.51	0.00
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 40	0	0	0.00	1.23	40.65	0.00
Salivary Gland Clontech	37.23, 39.21	8.45	2.5	5.48	7.31	6.84	37.45
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00

Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	40, 38.76	1.25	3.3	2.28	4.92	10.16	23.12
Stomach	40, 39.25	1.25	2.43	1.84	2.73	18.32	33.70
Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	37.82, 40	5.88	0	2.94	9.89	5.06	14.86
Thyroid	40, 40	0	0	0.00	2.77	18.05	0.00
Trachea Clontech	40, 40	0	0	0.00	9.71	5.15	0.00
Urinary Bladder	40, 40	0	0	0.00	5.47	9.14	0.00
Uterus	38.34, 40	4.27	0	2.14	5.34	9.36	19.99
genomic	29.66	888.99					
b-actin	30.72	462.87					
1.00E+05	22.2	100000					
1.00E+05	22.14	100000					
1.00E+04	25.72	10000					
1.00E+04	25.66	10000					
1.00E+03	29.16	1000					
1.00E+03	29.07	1000					
1.00E+02	32.37	100					
1.00E+02	34.12	100					
1.00E+01	37.12	10					
1.00E+01	37.11	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	38.03	-1					

Sample sbg995002PIGR	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detecte d/50 ng total RNA	Sample	Fold Change in Disease Populati on
colon normal GW98-167	21941	33.43	149.84	299.68	colon normal	
colon tumor GW98-166	21940	32.49	274.64	549.28	colon tumor	1.83
colon normal GW98-178	22080	40	0	0.00	colon normal	
colon tumor GW98-177	22060	31.11	675.8	1351.60	colon tumor	1351.60
colon normal GW98-561	23514	37.74	9.09	18.18	colon normal	
colon tumor GW98-560	23513	35.81	31.94	63.88	colon tumor	3.51
colon normal GW98-894	24691	33.17	177.11	354.22	colon normal	
colon tumor GW98-893	24690	31.61	488.49	976.98	colon tumor	2.76
lung normal GW98-3	20742	35.48	39.55	79.10	lung normal	
lung tumor GW98-2	20741	28.32	4121.56	8243.12	lung tumor	104.21
lung normal GW97-179	20677	36.47	20.69	41.38	lung normal	
lung tumor GW97-178	20676	37.24	12.59	25.18	lung tumor	-1.64
lung normal GW98-165	21922	37.32	11.96	23.92	lung normal	
lung tumor GW98-164	21921	36.07	26.9	53.80	lung tumor	2.25

lung normal GW98-282	22584	38.49	5.58	11.16	lung normal	
lung tumor GW98-281	22583	37.89	8.24	16.48	lung tumor	1.48
breast normal GW00-392	28750	39.03	3.93	3.93	breast normal	
breast tumor GW00-391	28746	38.01	7.65	15.30	breast tumor	3.89
breast normal GW00-413	28798	40	0	0.00	breast normal	
breast tumor GW00-412	28797	38.67	4.98	9.96	breast tumor	9.96
breast normal GW00-235:238	27592-95	40	0	0.00	breast normal	
breast tumor GW00-231:234	27588-91	40	0	0.00	breast tumor	0.00
breast normal GW98-621	23656	36.12	26.13	52.26	breast normal	
breast tumor GW98-620	23655	40	0	0.00	breast tumor	-52.26
brain normal BB99-542	25507	37.14	13.43	26.86	brain normal	
brain normal BB99-406	25509	40	0	0.00	brain normal	
brain normal BB99-904	25546	40	0	0.00	brain normal	
brain stage 5 ALZ BB99-874	25502	40	0	0.00	brain stage 5 ALZ	-8.95
brain stage 5 ALZ BB99-887	25503	40	0.51	1.02	brain stage 5 ALZ	-8.78
brain stage 5 ALZ BB99-862	25504	40	0.88	1.76	brain stage 5 ALZ	-5.09
brain stage 5 ALZ BB99-927	25542	40	1.9	3.80	brain stage 5 ALZ	-2.36
CT lung KC	normal	36.59	19.23	38.46	CT lung	
lung 26 KC	normal	40	0	0.00	lung 26	
lung 27 KC	normal	40	0	0.00	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-9.62
lung 28 KC	COPD	40	0	0.00	lung 28	-9.62
lung 23 KC	COPD	40	0	0.00	lung 23	-9.62
lung 25 KC	normal	40	0	0.00	lung 25	
asthmatic lung ODO3112	29321	40	0	0.00	asthmatic lung	-9.62
asthmatic lung ODO3433	29323	38.36	6.1	12.20	asthmatic lung	1.27
asthmatic lung ODO3397	29322	37.29	12.16	24.32	asthmatic lung	2.53
asthmatic lung ODO4928	29325	38.01	7.64	15.28	asthmatic lung	1.59
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		40	0	0.00	endo bFGF	0.00
heart Clontech	normal	37.85	8.49	16.98	heart	
heart (T-1) ischemic	29417	40	0	0.00	heart T-1	-16.98
heart (T-14) non-obstructive DCM	29422	40	0	0.00	heart T-14	-16.98
heart (T-3399) DCM	29426	39.5	2.9	5.80	heart T-3399	-2.93
adenoid GW99-269	26162	40	0	0.00	adenoid	
tonsil GW98-280	22582	36.35	22.46	44.92	tonsil	
T cells PC00314	28453	36.17	25.23	50.46	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0.45	0.90	monocyte	
B cells PC00665	28455	40	0.6	1.20	B cells	
dendritic cells 28441		38.07	7.37	14.74	dendritic cells	
neutrophils	28440	32.73	236.09	236.09	neutrophils	

eosinophils	28446	33.68	126.65	253.30	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim		36.52	20.1	20.10	BM stim	20.10
osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		39.61	2.7	6.75	chondrocytes	
OA Synovium IP12/01	29462	39.91	1.59	1.59	OA Synovium	
OA Synovium NP10/01	29461	38.98	4.07	8.14	OA Synovium	
OA Synovium NP57/00	28464	36.29	23.27	46.54	OA Synovium	
RA Synovium NP03/01	28466	35.81	31.94	63.88	RA Synovium	
RA Synovium NP71/00	28467	34.79	61.79	123.58	RA Synovium	
RA Synovium NP45/00	28475	35.08	51.15	102.30	RA Synovium	
OA bone (biobank)	29217	40	1.12	1.12	OA bone (biobank)	
OA bone Sample 1	J. Emory	36.8	16.77	33.54	OA bone	
OA bone Sample 2	J. Emory	34.72	64.74	129.48	OA bone	
Cartilage (pool)	Normal	37.46	10.93	21.86	Cartilage (pool)	
Cartilage (pool)	OA	40	0	0.00	Cartilage (pool)	-21.86
PBL uninfected	28441	35.05	52.27	104.54	PBL uninfected	
PBL HIV IIIB	28442	37.31	12.04	24.08	PBL HIV IIIB	-4.34
MRC5 uninfected (100%)	29158	40	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	38.19	6.8	13.60	MRC5 HSV strain F	13.60
W12 cells	29179	40	0	0.00	W12 cells	
Keratinocytes	29180	40	0	0.00	Keratinocytes	
B-actin control	B-actin control	29.77	1604.25			
genomic	genomic	30.5	1001.61			
1.00E+05	1.00E+05	22.95	100000			
1.00E+05	1.00E+05	22.91	100000			
1.00E+04	1.00E+04	26.49	10000			
1.00E+04	1.00E+04	26.66	10000			
1.00E+03	1.00E+03	30.62	1000			
1.00E+03	1.00E+03	30.43	1000			
1.00E+02	1.00E+02	36.12	100			
1.00E+02	1.00E+02	34.73	100			
1.00E+01	1.00E+01	38.58	10			
1.00E+01	1.00E+01	38.82	10			
1.00E-00	1.00E-00	40	0			
1.00E-00	1.00E-00	37.86	1			
NTC	NTC	40	0			

Gene Name sbg995002PIGR

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.83

colon tumor	1351.60
colon tumor	3.51
colon tumor	2.76
lung tumor	104.21
lung tumor	-1.64
lung tumor	2.25
lung tumor	1.48
breast tumor	3.89
breast tumor	9.96
breast tumor	0.00
breast tumor	-52.26
brain stage 5 ALZ	-8.95
brain stage 5 ALZ	-8.78
brain stage 5 ALZ	-5.09
brain stage 5 ALZ	-2.36
lung 24	-9.62
lung 28	-9.62
lung 23	-9.62
asthmatic lung	-9.62
asthmatic lung	1.27
asthmatic lung	2.53
asthmatic lung	1.59
endo VEGF	0.00
endo bFGF	0.00
heart T-1	-16.98
heart T-14	-16.98
heart T-3399	-2.93
BM stim	20.10
osteo dif	0.00
Cartilage (pool)	-21.86
PBL HIV IIIB	-4.34
MRC5 HSV strain F	13.60

Gene Name sbg1033026C1q

5 Low to moderate overall expression in normal and disease samples. Highest normal expression in the subcutaneous adipocytes, subcutaneous adipose, whole brain, and heart. Highest disease expression in the 3 heart samples. Downregulation in 1 of 4 lung tumor samples and upregulation in 2 of 4 breast tumor samples indicates a role for this gene in cancers of the lung and breast. Upregulation in 2 of 4 AD brain samples suggests an involvement in Alzheimer's disease. Upregulation in 3 of 3 heart samples implies an involvement in cardiovascular diseases such as non-obstructive and obstructive DCM as well as ischemia. Low expression in all of the immune cells. Low to moderate expression in the OA synovium and bone samples as well as in the RA synovium samples.

Sample sbg1033026C1q	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/50 ng total RNA
Subcutaneous Adipocytes Zenbio	32.32, 31.18	11.99	24.91	18.45	3.06	16.34	301.47
Subcutaneous Adipose Zenbio	34.95, 33.78	2.2	4.69	3.45	0.96	52.36	180.37

Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	28.5, 28.04	140.11	187.98	164.05	7.24	6.91	1132.91
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	40, 40	0	0	0.00	2.17	23.04	0.00
Cervix	40, 40	0	0	0.00	2.42	20.66	0.00
Colon	34.82, 38.44	2.39	0.23	1.31	2.71	18.45	24.17
Endometrium	40, 35.09	0	2.01	1.01	0.73	68.21	68.55
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	32.53, 34.31	10.45	3.32	6.89	1.32	37.88	260.80
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	40, 34.55	0	2.85	1.43	2.58	19.38	27.62
Jejunum	33.04, 34.86	7.51	2.33	4.92	6.60	7.58	37.27
Kidney	40, 40	0	0	0.00	2.12	23.58	0.00
Liver	35.81, 33.92	1.26	4.28	2.77	1.50	33.33	92.33
Fetal Liver Clontech	32.05, 40	14.25	0	7.13	10.40	4.81	34.25
Lung	40, 33.51	0	5.58	2.79	2.57	19.46	54.28
Mammary Gland Clontech	31.05, 30.69	27.02	34.2	30.61	13.00	3.85	117.73
Myometrium	33.29, 35.1	6.42	2	4.21	2.34	21.37	89.96
Omentum	34.44, 40	3.07	0	1.54	3.94	12.69	19.48
Ovary	32.59, 35.04	10.03	2.07	6.05	4.34	11.52	69.70
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	34.63, 33.09	2.71	7.29	5.00	5.48	9.12	45.62
Placenta Clontech	32.77, 33.01	8.94	7.7	8.32	5.26	9.51	79.09
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 34.44	0	3.06	1.53	1.23	40.65	62.20
Salivary Gland Clontech	32.96, 40	7.94	0	3.97	7.31	6.84	27.15
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	40, 33.46	0.6	5.75	3.18	1.21	41.32	131.20
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	35.65, 35	1.4	2.13	1.77	4.92	10.16	17.94
Stomach	40, 34.73	0	2.54	1.27	2.73	18.32	23.26
Testis Clontech	40, 35.12	0	1.98	0.99	0.57	87.87	86.99
Thymus Clontech	32.44, 31.57	11.11	19.37	15.24	9.89	5.06	77.05
Thyroid	40, 40	0	0	0.00	2.77	18.05	0.00
Trachea Clontech	34.58, 33.56	2.79	5.4	4.10	9.71	5.15	21.09
Urinary Bladder	33.45, 33.34	5.8	6.21	6.01	5.47	9.14	54.89
Uterus	33.19, 32.41	6.82	11.32	9.07	5.34	9.36	84.93
genomic	25.47	981.57					
b-actin	26.87	398.61					
1.00E+05	18.24	100000					
1.00E+05	18.35	100000					
1.00E+04	21.53	10000					
1.00E+04	21.62	10000					

1.00E+03	25.17	1000					
1.00E+03	25.03	1000					
1.00E+02	30.53	100					
1.00E+02	30.49	100					
1.00E+01	30.85	10					
1.00E+01	40	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg1033026C1q	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detecte d/50 ng total RNA	Sample	Fold Change in Disease Populat ion
colon normal GW98-167	21941	27.03	397.15	794.30	colon normal	
colon tumor GW98-166	21940	29.53	91.39	182.78	colon tumor	-4.35
colon normal GW98-178	22080	30.3	57.81	115.62	colon normal	
colon tumor GW98-177	22060	29.31	103.84	207.68	colon tumor	1.80
colon normal GW98-561	23514	28.79	140.64	281.28	colon normal	
colon tumor GW98-560	23513	30.18	62.18	124.36	colon tumor	-2.26
colon normal GW98-894	24691	28.31	187.28	374.56	colon normal	
colon tumor GW98-893	24690	28.75	143.93	287.86	colon tumor	-1.30
lung normal GW98-3	20742	28.18	201.78	403.56	lung normal	
lung tumor GW98-2	20741	32.35	17.41	34.82	lung tumor	-11.59
lung normal GW97-179	20677	29.94	71.52	143.04	lung normal	
lung tumor GW97-178	20676	28.76	143.36	286.72	lung tumor	2.00
lung normal GW98-165	21922	28.69	149.49	298.98	lung normal	
lung tumor GW98-164	21921	31.28	32.63	65.26	lung tumor	-4.58
lung normal GW98-282	22584	31.42	30.07	60.14	lung normal	
lung tumor GW98-281	22583	30.33	56.83	113.66	lung tumor	1.89
breast normal GW00-392	28750	28.72	146.7	146.70	breast normal	
breast tumor GW00-391	28746	27.02	398.56	797.12	breast tumor	5.43
breast normal GW00-413	28798	30.95	39.63	39.63	breast normal	
breast tumor GW00-412	28797	30.58	49.03	98.06	breast tumor	2.47
breast normal GW00-235:238	27592-95	32.53	15.6	15.60	breast normal	
breast tumor GW00-231:234	27588-91	29.58	88.49	88.49	breast tumor	5.67
breast normal GW98-621	23656	27.5	300.39	600.78	breast normal	
breast tumor GW98-620	23655	29.28	105.43	210.86	breast tumor	-2.85
brain normal BB99-542	25507	30.67	46.59	93.18	brain normal	
brain normal BB99-406	25509	29.54	90.66	181.32	brain normal	
brain normal BB99-904	25546	31.13	35.58	71.16	brain normal	
brain stage 5 ALZ BB99-874	25502	31.4	30.36	60.72	brain stage 5 ALZ	-1.90

brain stage 5 ALZ BB99-887	25503	28.39	177.94	355.88	brain stage 5 ALZ	3.09
brain stage 5 ALZ BB99-862	25504	28.92	130.19	260.38	brain stage 5 ALZ	2.26
brain stage 5 ALZ BB99-927	25542	28.2	198.98	397.96	brain stage 5 ALZ	3.45
CT lung KC	normal	31.24	33.37	66.74	CT lung	
lung 26 KC	normal	33.59	8.37	8.37	lung 26	
lung 27 KC	normal	37.8	0.7	0.70	lung 27	
lung 24 KC	COPD	34.56	4.73	4.73	lung 24	-4.39
lung 28 KC	COPD	35.39	2.91	2.91	lung 28	-7.13
lung 23 KC	COPD	34.74	4.26	4.26	lung 23	-4.87
lung 25 KC	normal	33.85	7.19	7.19	lung 25	
asthmatic lung ODO3112	29321	35.04	3.57	3.57	asthmatic lung	-5.81
asthmatic lung ODO3433	29323	32.44	16.48	32.96	asthmatic lung	1.59
asthmatic lung ODO3397	29322	29.4	98.44	196.88	asthmatic lung	9.49
asthmatic lung ODO4928	29325	31.1	36.23	72.46	asthmatic lung	3.49
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		35.4	2.89	2.89	endo bFGF	2.89
heart Clontech	normal	29.05	120.78	241.56	heart	
heart (T-1) ischemic	29417	26.23	633.79	1267.58	heart T-1	5.25
heart (T-14) non-obstructive DCM	29422	25.74	847.85	1695.70	heart T-14	7.02
heart (T-3399) DCM	29426	25.03	1289.37	2578.74	heart T-3399	10.68
adenoid GW99-269	26162	35.24	3.17	6.34	adenoid	
tonsil GW98-280	22582	31	38.35	76.70	tonsil	
T cells PC00314	28453	31.75	24.69	49.38	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	31.35	31.31	62.62	B cells	
dendritic cells 28441		32.81	13.25	26.50	dendritic cells	
neutrophils	28440	31.76	24.51	24.51	neutrophils	
eosinophils	28446	33.08	11.29	22.58	eosinophils	
BM unstim		36.9	1.19	1.19	BM unstim	
BM stim		38.86	0.38	0.38	BM stim	-3.13
osteo dif		37.77	0.72	0.72	osteo dif	0.72
osteo undif		40	0	0.00	osteo undif	
chondrocytes		33.14	10.88	27.20	chondrocytes	
OA Synovium IP12/01	29462	30.61	48.28	48.28	OA Synovium	
OA Synovium NP10/01	29461	27.5	300.97	601.94	OA Synovium	
OA Synovium NP57/00	28464	29.28	105.55	211.10	OA Synovium	
RA Synovium NP03/01	28466	30.18	62.3	124.60	RA Synovium	
RA Synovium NP71/00	28467	29.22	109.5	219.00	RA Synovium	
RA Synovium NP45/00	28475	30.06	66.71	133.42	RA Synovium	
OA bone (biobank)	29217	32.6	14.99	14.99	OA bone (biobank)	
OA bone Sample 1	J. Emory	30.48	52.25	104.50	OA bone	
OA bone Sample 2	J. Emory	32.31	17.76	35.52	OA bone	
Cartilage (pool)	Normal	30.45	53.05	106.10	Cartilage (pool)	

Cartilage (pool)	OA	30.81	43.01	86.02	Cartilage (pool)	-1.23
PBL uninfected	28441	30.19	61.92	123.84	PBL uninfected	
PBL HIV IIIB	28442	31.19	34.35	68.70	PBL HIV IIIB	-1.80
MRC5 uninfected (100%)	29158	30.19	62.02	124.04	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	31.13	35.48	70.96	MRC5 HSV strain F	-1.75
W12 cells	29179	32	21.32	42.64	W12 cells	
Keratinocytes	29180	33.3	9.92	19.84	Keratinocytes	
B-actin control		26.66	492.23			
genomic		24.83	1443.91			
1.00E+05		18.12	100000			
1.00E+05		18.12	100000			
1.00E+04		21.28	10000			
1.00E+04		21.31	10000			
1.00E+03		24.92	1000			
1.00E+03		24.9	1000			
1.00E+02		29.22	100			
1.00E+02		29.26	100			
1.00E+01		33.13	10			
1.00E+01		34.32	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg1033026C1q

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-4.35
colon tumor	1.80
colon tumor	-2.26
colon tumor	-1.30
lung tumor	-11.59
lung tumor	2.00
lung tumor	-4.58
lung tumor	1.89
breast tumor	5.43
breast tumor	2.47
breast tumor	5.67
breast tumor	-2.85
brain stage 5 ALZ	-1.90
brain stage 5 ALZ	3.09
brain stage 5 ALZ	2.26
brain stage 5 ALZ	3.45
lung 24	-4.39
lung 28	-7.13
lung 23	-4.87
asthmatic lung	-5.81
asthmatic lung	1.59
asthmatic lung	9.49

asthmatic lung	3.49
endo VEGF	0.00
endo bFGF	2.89
heart T-1	5.25
heart T-14	7.02
heart T-3399	10.68
BM stim	-3.13
osteo dif	0.72
Cartilage (pool)	-1.23
PBL HIV IIIB	-1.80
MRC5 HSV strain F	-1.75

Gene Name sbg1003675Rnase

FAILED

5

Gene Name sbg1015258PLM

Low overall expression in normal and disease samples. Highest normal expression in the endometrium, hypothalamus, liver small intestine, and the testis. Highest disease expression in one of the breast normal/tumor pairs, one of the normal brain samples, two of the Alzheimer's disease brain samples, the B cells and the HSV-infected MRC5 cells. Downregulation in 1 of 4 lung tumor samples is sufficient to claim a role in cancer of the lung. Upregulation in 2 of 4 breast tumor samples indicates an involvement in cancer of the breast. Downregulation in 2 of 3 COPD samples and in 1 of 4 asthmatic lung samples implies a role in chronic obstructive pulmonary disease and asthma. Upregulation in the obstructive DCM heart sample suggests a potential role in cardiovascular disease. Downregulation in the stimulated bone marrow sample. Downregulation in the OA cartilage pool implicates this gene in osteoarthritis. Upregulation in the HSV-infected MRC5 cells suggests that this gene may be a host factor in HSV. Low expression in all immune cells except the B cells which show moderate expression.

Sample sbg1015258PLM	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	39.96, 39.32	0.39	0.73	0.56	3.06	16.34	9.15
Subcutaneous Adipose Zenbio	39.61, 37.77	0.62	1.84	1.23	0.96	52.36	64.40
Adrenal Gland Clontech	36.89, 37.65	3.12	1.98	2.55	0.61	81.97	209.02
Whole Brain Clontech	32.77, 33.06	36.18	30.37	33.28	7.24	6.91	229.80
Fetal Brain Clontech	38.01, 37.52	1.6	2.14	1.87	0.48	103.95	194.39
Cerebellum Clontech	38.34, 37.8	1.31	1.81	1.56	2.17	23.04	35.94
Cervix	36.9, 37.17	3.1	2.64	2.87	2.42	20.66	59.30
Colon	35.93, 37.95	5.51	1.66	3.59	2.71	18.45	66.14
Endometrium	34.62, 37.51	12.02	2.15	7.09	0.73	68.21	483.29
Esophagus	35.76, 37.39	6.1	2.31	4.21	1.37	36.50	153.47
Heart Clontech	36.78, 38.53	3.33	1.17	2.25	1.32	37.88	85.23
Hypothalamus	37.12, 36.52	2.71	3.87	3.29	0.32	155.28	510.87
Ileum	36.15, 36.19	4.84	4.72	4.78	2.58	19.38	92.64
Jejunum	34.6, 33.48	12.14	23.65	17.90	6.60	7.58	135.57
Kidney	37.16, 37.9	2.65	1.7	2.18	2.12	23.58	51.30

Liver	34.6, 36.06	12.13	5.11	8.62	1.50	33.33	287.33
Fetal Liver Clontech	34.32, 36.91	14.35	3.07	8.71	10.40	4.81	41.88
Lung	36.94, 35.31	3.02	7.98	5.50	2.57	19.46	107.00
Mammary Gland Clontech	38.03, 36.89	1.58	3.11	2.35	13.00	3.85	9.02
Myometrium	38.44, 38	1.24	1.6	1.42	2.34	21.37	30.34
Omentum	35.41, 35.38	7.51	7.64	7.58	3.94	12.69	96.13
Omentum							
Ovary	34.32, 34.36	14.4	14.07	14.24	4.34	11.52	164.00
Pancreas	36.44, 36.82	4.07	3.25	3.66	0.81	61.80	226.21
Head of Pancreas	37.54, 36.96	2.11	2.98	2.55	1.57	31.85	81.05
Parotid Gland	37.1, 35.46	2.75	7.29	5.02	5.48	9.12	45.80
Placenta Clontech	36.07, 35.36	5.08	7.74	6.41	5.26	9.51	60.93
Prostate	37.4, 37.82	2.3	1.79	2.05	3.00	16.67	34.08
Rectum	36.65, 37.39	3.59	2.32	2.96	1.23	40.65	120.12
Salivary Gland Clontech	38.55, 39.31	1.16	0.74	0.95	7.31	6.84	6.50
Skeletal Muscle Clontech	37.59, 36.87	2.06	3.15	2.61	1.26	39.68	103.37
Skin	38.36, 36.33	1.3	4.34	2.82	1.21	41.32	116.53
Small Intestine Clontech	36.05, 36.76	5.14	3.37	4.26	0.98	51.07	217.31
Spleen	37.62, 35.34	2.02	7.83	4.93	4.92	10.16	50.05
Stomach	35.8, 35.15	5.95	8.76	7.36	2.73	18.32	134.71
Testis Clontech	35.14, 37.08	8.82	2.77	5.80	0.57	87.87	509.23
Thymus Clontech	35.89, 35.06	5.65	9.22	7.44	9.89	5.06	37.59
Thyroid	37.59, 37.2	2.06	2.59	2.33	2.77	18.05	41.97
Trachea Clontech	37.52, 37.95	2.14	1.66	1.90	9.71	5.15	9.78
Urinary Bladder	37.47, 35.44	2.2	7.38	4.79	5.47	9.14	43.78
Uterus	34.17, 34.12	15.66	16.17	15.92	5.34	9.36	149.02
genomic	27.03	1097.52					
b-actin	27.23	974.77					
1.00E+05	19.25	100000					
1.00E+05	19.2	100000					
1.00E+04	22.99	10000					
1.00E+04	22.94	10000					
1.00E+03	27.09	1000					
1.00E+03	27.28	1000					
1.00E+02	31.49	100					
1.00E+02	31.46	100					
1.00E+01	37.86	10					
1.00E+01	35.45	10					
1.00E-00	37.08	1					
1.00E-00	37.4	1					
NTC	36.45	-1					
NTC	36.15	-1					

Sample sbg1015258PLM	Reg number	Ct	Mean GOI	copies of mRNA	Sample	Fold Change in
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	(GSK identifier)		copies	detected/ 50 ng total RNA		Disease Population
colon normal GW98-167	21941	35.4	9.91	19.82	colon normal	
colon tumor GW98-166	21940	35.13	11.61	23.22	colon tumor	1.17
colon normal GW98-178	22080	34.84	13.83	27.66	colon normal	
colon tumor GW98-177	22060	35	12.59	25.18	colon tumor	-1.10
colon normal GW98-561	23514	35.48	9.4	18.80	colon normal	
colon tumor GW98-560	23513	36.2	6.14	12.28	colon tumor	-1.53
colon normal GW98-894	24691	34.53	16.62	33.24	colon normal	
colon tumor GW98-893	24690	34.29	19.25	38.50	colon tumor	1.16
lung normal GW98-3	20742	34.53	16.69	33.38	lung normal	
lung tumor GW98-2	20741	37.87	2.25	4.50	lung tumor	-7.42
lung normal GW97-179	20677	34.59	16.02	32.04	lung normal	
lung tumor GW97-178	20676	34.45	17.43	34.86	lung tumor	1.09
lung normal GW98-165	21922	33.89	24.39	48.78	lung normal	
lung tumor GW98-164	21921	35.48	9.43	18.86	lung tumor	-2.59
lung normal GW98-282	22584	36.67	4.62	9.24	lung normal	
lung tumor GW98-281	22583	37.87	2.26	4.52	lung tumor	-2.04
breast normal GW00-392	28750	34.17	20.64	20.64	breast normal	
breast tumor GW00-391	28746	33.54	30.09	60.18	breast tumor	2.92
breast normal GW00-413	28798	39.05	1.11	1.11	breast normal	
breast tumor GW00-412	28797	35.01	12.46	24.92	breast tumor	22.45
breast normal GW00-235:238	27592-95	40	0.55	0.55	breast normal	
breast tumor GW00-231:234	27588-91	35.07	12.02	12.02	breast tumor	21.85
breast normal GW98-621	23656	33	41.58	83.16	breast normal	
breast tumor GW98-620	23655	33.05	40.47	80.94	breast tumor	-1.03
brain normal BB99-542	25507	32.73	48.93	97.86	brain normal	
brain normal BB99-406	25509	33.97	23.34	46.68	brain normal	
brain normal BB99-904	25546	37.88	2.24	4.48	brain normal	
brain stage 5 ALZ BB99-874	25502	35.92	7.25	14.50	brain stage 5 ALZ	-3.43
brain stage 5 ALZ BB99-887	25503	31.57	97.99	195.98	brain stage 5 ALZ	3.95
brain stage 5 ALZ BB99-862	25504	36.08	6.57	13.14	brain stage 5 ALZ	-3.78
brain stage 5 ALZ BB99-927	25542	32.66	50.98	101.96	brain stage 5 ALZ	2.05
CT lung KC	normal	37.37	3.04	6.08	CT lung	
lung 26 KC	normal				lung 26	
lung 27 KC	normal	38.52	1.52	1.52	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-3.07
lung 28 KC	COPD	37.4	2.99	2.99	lung 28	-1.03
lung 23 KC	COPD	39.56	0.82	0.82	lung 23	-3.74
lung 25 KC	normal	38.43	1.61	1.61	lung 25	

asthmatic lung ODO3112	29321	39.45	0.88	0.88	asthmatic lung	-3.49
asthmatic lung ODO3433	29323	36.48	5.19	10.38	asthmatic lung	3.38
asthmatic lung ODO3397	29322	35.56	8.99	17.98	asthmatic lung	5.86
asthmatic lung ODO4928	29325	37.06	3.66	7.32	asthmatic lung	2.38
endo cells KC	control	39.29	0.96	0.96	endo cells	
endo VEGF KC		37.65	2.57	2.57	endo VEGF	2.68
endo bFGF KC		40	0.48	0.48	endo bFGF	-2.00
heart Clontech	normal	40	0.68	1.36	heart	
heart (T-1) ischemic	29417	39.29	0.96	1.92	heart T-1	1.41
heart (T-14) non- obstructive DCM	29422	38.21	1.84	3.68	heart T-14	2.71
heart (T-3399) DCM	29426	35.49	9.35	18.70	heart T-3399	13.75
adenoid GW99-269	26162	39.63	0.78	1.56	adenoid	
tonsil GW98-280	22582	34.5	16.92	33.84	tonsil	
T cells PC00314	28453	34.57	16.25	32.50	T cells	
PBMNC		37.32	3.13	3.13	PBMNC	
monocyte		37.74	2.44	4.88	monocyte	
B cells PC00665	28455	33.32	34.36	68.72	B cells	
dendritic cells 28441		37.29	3.19	6.38	dendritic cells	
neutrophils	28440	36.01	6.85	6.85	neutrophils	
eosinophils	28446	35.38	9.98	19.96	eosinophils	
BM unstim		37.44	2.91	2.91	BM unstim	
BM stim		40	0.53	0.53	BM stim	-5.49
osteo dif		38.15	1.91	1.91	osteo dif	-1.38
osteo undif		37.6	2.64	2.64	osteo undif	
chondrocytes		36.1	6.51	16.28	chondrocytes	
OA Synovium IP12/01	29462	35.58	8.86	8.86	OA Synovium	
OA Synovium NP10/01	29461	35.46	9.54	19.08	OA Synovium	
OA Synovium NP57/00	28464	34.05	22.23	44.46	OA Synovium	
RA Synovium NP03/01	28466	37.92	2.19	4.38	RA Synovium	
RA Synovium NP71/00	28467	35.39	9.92	19.84	RA Synovium	
RA Synovium NP45/00	28475	35.03	12.37	24.74	RA Synovium	
OA bone (biobank)	29217	39.98	0.67	0.67	OA bone (biobank)	
OA bone Sample 1	J. Emory	36.06	6.68	13.36	OA bone	
OA bone Sample 2	J. Emory	39.89	0.67	1.34	OA bone	
Cartilage (pool)	Normal	35.57	8.92	17.84	Cartilage (pool)	
Cartilage (pool)	OA	39.5	0.85	1.70	Cartilage (pool)	-10.49
PBL uninfected	28441	36.65	4.67	9.34	PBL uninfected	
PBL HIV IIIB	28442	36.94	3.92	7.84	PBL HIV IIIB	-1.19
MRC5 uninfected (100%)	29158	37.54	2.74	5.48	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	33.19	37.18	74.36	MRC5 HSV strain F	13.57
W12 cells	29179	37.23	3.3	6.60	W12 cells	
Keratinocytes	29180	37.18	3.4	6.80	Keratinocytes	

B-actin control		27.26	1296.87			
genomic		27.2	1345.34			
1.00E+05		19.44	100000			
1.00E+05		19.81	100000			
1.00E+04		23.63	10000			
1.00E+04		23.41	10000			
1.00E+03		27.77	1000			
1.00E+03		27.89	1000			
1.00E+02		32.32	100			
1.00E+02		32.3	100			
1.00E+01		36.77	10			
1.00E+01		36.39	10			
1.00E-00		38.06	1			
1.00E-00		37.56	1			
NTC		38.18	-1			

Gene Name sbg1015258PLM

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.17
colon tumor	-1.10
colon tumor	-1.53
colon tumor	1.16
lung tumor	-7.42
lung tumor	1.09
lung tumor	-2.59
lung tumor	-2.04
breast tumor	2.92
breast tumor	22.45
breast tumor	21.85
breast tumor	-1.03
brain stage 5 ALZ	-3.43
brain stage 5 ALZ	3.95
brain stage 5 ALZ	-3.78
brain stage 5 ALZ	2.05
lung 24	-3.07
lung 28	-1.03
lung 23	-3.74
asthmatic lung	-3.49
asthmatic lung	3.38
asthmatic lung	5.86
asthmatic lung	2.38
endo VEGF	2.68
endo bFGF	-2.00

heart T-1	1.41
heart T-14	2.71
heart T-3399	13.75
BM stim	-5.49
osteo dif	-1.38
Cartilage (pool)	-10.49
PBL HIV IIIB	-1.19
MRC5 HSV strain F	13.57

Gene Name sbg1003328IG (Taqman)

5 Moderate overall expression. Highest normal expression in whole brain, fetal brain, and cerebellum with slightly lower levels of expression in the colon and mammary gland. Highest disease expression in the colon and lung tumor pairs as well as the normal and Alzheimer's brain. Significant upregulation in 2 of 4 breast tumor samples with slight upregulation in 1 of 4 breast tumor samples implicates this gene in breast cancer. Downregulation in 3 of 3 COPD samples may suggest an involvement in chronic obstructive pulmonary disease. Downregulation in 1 of 4 asthma samples suggests a potential role for this gene in asthma. Downregulation in the HSV-infected MRC5 cells suggests that this gene may play a role in HSV. High expression in 3 of 3 OA synovium samples, 3 of 3 RA synovium samples, 2 of 2 OA bone samples, and corroborating high expression in the T cells and B cells implicates this gene in osteoarthritis and rheumatoid arthritis.

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Sample sbg1003328IG	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected /50 ng total RNA
Subcutaneous Adipocytes Zenbio	32.35, 32.1	109.15	127.12	118.14	3.06	16.34	1930.31
Subcutaneous Adipose Zenbio	37.92, 40	3.84	0	1.92	0.96	52.36	100.52
Adrenal Gland Clontech	38.07, 35.73	3.5	14.32	8.91	0.61	81.97	730.33
Whole Brain Clontech	22.72, 23.09	35640.5	28576.52	32108.51	7.24	6.91	221743.85
Fetal Brain Clontech	33.39, 34.06	58.43	39.04	48.74	0.48	103.95	5066.01
Cerebellum Clontech	31.32, 31.02	202.49	242.95	222.72	2.17	23.04	5131.80
Cervix	36.36, 35.6	9.78	15.49	12.64	2.42	20.66	261.05
Colon	30.74, 32.11	286.9	125.78	206.34	2.71	18.45	3807.01
Endometrium	34.58, 36.01	28.47	12.11	20.29	0.73	68.21	1384.04
Esophagus	37.54, 36.05	4.82	11.78	8.30	1.37	36.50	302.92
Heart Clontech	36.23, 36.85	10.56	7.3	8.93	1.32	37.88	338.26
Hypothalamus	40, 36.96	0	6.81	3.41	0.32	155.28	528.73
Ileum	34.79, 34.48	25.09	30.4	27.75	2.58	19.38	537.69
Jejunum	30.14, 31.02	412.72	242.47	327.60	6.60	7.58	2481.78
Kidney	33.94, 34.61	41.89	28.12	35.01	2.12	23.58	825.59
Liver	36.11, 35.38	11.41	17.61	14.51	1.50	33.33	483.67
Fetal Liver Clontech	30.24, 30.27	388.12	381.28	384.70	10.40	4.81	1849.52
Lung	35.59, 35.09	15.59	20.98	18.29	2.57	19.46	355.74
Mammary Gland Clontech	29.21, 28.52	718.74	1090.18	904.46	13.00	3.85	3478.69

Myometrium	33.7, 34.11	48.42	37.85	43.14	2.34	21.37	921.69
Omentum	33.83, 33.57	44.75	52.27	48.51	3.94	12.69	615.61
Ovary	32.47, 32.34	101.42	109.96	105.69	4.34	11.52	1217.63
Pancreas	38.16, 40	3.31	0	1.66	0.81	61.80	102.29
Head of Pancreas	40, 36.68	0	8.07	4.04	1.57	31.85	128.50
Parotid Gland	31.68, 31.03	162.92	241.11	202.02	5.48	9.12	1843.20
Placenta Clontech	30.48, 30.82	335.37	274.53	304.95	5.26	9.51	2898.76
Prostate	33.39, 32.15	58.39	122.82	90.61	3.00	16.67	1510.08
Rectum	35.95, 35.32	12.5	18.32	15.41	1.23	40.65	626.42
Salivary Gland Clontech	31.25, 30.65	211.88	303.2	257.54	7.31	6.84	1761.56
Skeletal Muscle Clontech	36.61, 37.62	8.44	4.6	6.52	1.26	39.68	258.73
Skin	36.37, 36.08	9.71	11.56	10.64	1.21	41.32	439.46
Small Intestine Clontech	36.74, 34.51	7.79	29.79	18.79	0.98	51.07	959.65
Spleen	34.78, 35.63	25.25	15.18	20.22	4.92	10.16	205.44
Stomach	40, 35.13	0.88	20.56	10.72	2.73	18.32	196.34
Testis Clontech	35.01, 39.68	22.07	1.33	11.70	0.57	87.87	1028.12
Thymus Clontech	29.15, 29.2	749.23	724.61	736.92	9.89	5.06	3725.58
Thyroid	32.02, 32.14	133.23	123.77	128.50	2.77	18.05	2319.49
Trachea Clontech	31.28, 30.17	207.67	405.04	306.36	9.71	5.15	1577.52
Urinary Bladder	33.07, 32.91	70.6	78.07	74.34	5.47	9.14	679.48
Uterus	33.01, 33.15	73.56	67.48	70.52	5.34	9.36	660.30
genomic	29.15	746.77					
b-actin	30.2	397.52					
1.00E+05	21.06	100000					
1.00E+05	20.94	100000					
1.00E+04	25.06	10000					
1.00E+04	24.54	10000					
1.00E+03	28.32	1000					
1.00E+03	28.77	1000					
1.00E+02	33	100					
1.00E+02	32.74	100					
1.00E+01	35.9	10					
1.00E+01	40	0					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg1003328IG	Reg number (GSK identifie r)	Ct	Mean GOI copies	copies of mRNA detected/ 50 ng total RNA	Sample	Fold Change in Disease Populati on
colon normal GW98-167	21941	24.26	15509.01	31018.02	colon normal	

colon tumor GW98-166	21940	24.5	13727.44	27454.88	colon tumor	-1.13
colon normal GW98-178	22080	28.01	2276.97	4553.94	colon normal	
colon tumor GW98-177	22060	27.11	3618.2	7236.40	colon tumor	1.59
colon normal GW98-561	23514	24.47	13993.67	27987.34	colon normal	
colon tumor GW98-560	23513	25.32	9040.47	18080.94	colon tumor	-1.55
colon normal GW98-894	24691	24.17	16251.61	32503.22	colon normal	
colon tumor GW98-893	24690	25.15	9872.46	19744.92	colon tumor	-1.65
lung normal GW98-3	20742	24.4	14498.52	28997.04	lung normal	
lung tumor GW98-2	20741	24.66	12640.32	25280.64	lung tumor	-1.15
lung normal GW97-179	20677	24.12	16680.84	33361.68	lung normal	
lung tumor GW97-178	20676	24.69	12468.91	24937.82	lung tumor	-1.34
lung normal GW98-165	21922	25.09	10168.18	20336.36	lung normal	
lung tumor GW98-164	21921	25.49	8296.37	16592.74	lung tumor	-1.23
lung normal GW98-282	22584	26.85	4131.52	8263.04	lung normal	
lung tumor GW98-281	22583	26.59	4702	9404.00	lung tumor	1.14
breast normal GW00-392	28750	25.9	6719.98	6719.98	breast normal	
breast tumor GW00-391	28746	25.04	10402.11	20804.22	breast tumor	3.10
breast normal GW00-413	28798	32.51	226.94	226.94	breast normal	
breast tumor GW00-412	28797	26.37	5261.73	10523.46	breast tumor	46.37
breast normal GW00-235:238	27592-95	34.58	78.63	78.63	breast normal	
breast tumor GW00-231:234	27588-91	28.45	1812.86	1812.86	breast tumor	23.06
breast normal GW98-621	23656	25.26	9289.36	18578.72	breast normal	
breast tumor GW98-620	23655	25.66	7579.13	15158.26	breast tumor	-1.23
brain normal BB99-542	25507	22.52	37845.47	75690.94	brain normal	
brain normal BB99-406	25509	23.07	28574.8	57149.60	brain normal	
brain normal BB99-904	25546	23.85	19214.49	38428.98	brain normal	
brain stage 5 ALZ BB99-874	25502	25.98	6442.51	12885.02	brain stage 5 ALZ	-4.43
brain stage 5 ALZ BB99-887	25503	23.19	26936.06	53872.12	brain stage 5 ALZ	-1.06
brain stage 5 ALZ BB99-862	25504	23.42	23948.83	47897.66	brain stage 5 ALZ	-1.19
brain stage 5 ALZ BB99-927	25542	24.15	16419.33	32838.66	brain stage 5 ALZ	-1.74
CT lung KC	normal	25.63	7714.35	15428.70	CT lung	
lung 26 KC	normal	32.34	247.99	247.99	lung 26	
lung 27 KC	normal	33.71	122.77	122.77	lung 27	
lung 24 KC	COPD	32.47	231.47	231.47	lung 24	-17.21
lung 28 KC	COPD	32.63	213.14	213.14	lung 28	-18.70
lung 23 KC	COPD	31.2	444.95	444.95	lung 23	-8.96
lung 25 KC	normal	33.46	139.4	139.40	lung 25	
asthmatic lung ODO3112	29321	31.6	360.95	360.95	asthmatic lung	-11.04
asthmatic lung ODO3433	29323	28.66	1634.71	3269.42	asthmatic lung	-1.22
asthmatic lung	29322	26.36	5294.26	10588.52	asthmatic lung	2.66

ODO3397						
asthmatic lung ODO4928	29325	28.23	2033.93	4067.86	asthmatic lung	1.02
endo cells KC	control	30.68	580.47	580.47	endo cells	
endo VEGF KC		31.08	471.26	471.26	endo VEGF	-1.23
endo bFGF KC		32.25	259.04	259.04	endo bFGF	-2.24
heart Clontech	normal	27.28	3312.82	6625.64	heart	
heart (T-1) ischemic	29417	27.48	2979.22	5958.44	heart T-1	-1.11
heart (T-14) non- obstructive DCM	29422	27.74	2613.8	5227.60	heart T-14	-1.27
heart (T-3399) DCM	29426	26.66	4541.38	9082.76	heart T-3399	1.37
adenoid GW99-269	26162	27.83	2493.31	4986.62	adenoid	
tonsil GW98-280	22582	25.68	7506.04	15012.08	tonsil	
T cells PC00314	28453	27.18	3487.61	6975.22	T cells	
PBMNC		32.6	216.73	216.73	PBMNC	
monocyte		32.27	256.89	513.78	monocyte	
B cells PC00665	28455	27.83	2492.12	4984.24	B cells	
dendritic cells 28441		26.67	4528.97	9057.94	dendritic cells	
neutrophils	28440	28.4	1862.35	1862.35	neutrophils	
eosinophils	28446	31.69	344.59	689.18	eosinophils	
BM unstim		32.04	289.03	289.03	BM unstim	
BM stim		30.59	607.18	607.18	BM stim	2.10
osteo dif		28.43	1831.57	1831.57	osteo dif	3.42
osteo undif		30.83	536	536.00	osteo undif	
chondrocytes		26.74	4368.46	10921.15	chondrocytes	
OA Synovium IP12/01	29462	27.91	2391.03	2391.03	OA Synovium	
OA Synovium NP10/01	29461	27.4	3109.93	6219.86	OA Synovium	
OA Synovium NP57/00	28464	27.05	3729.47	7458.94	OA Synovium	
RA Synovium NP03/01	28466	25.53	8116.96	16233.92	RA Synovium	
RA Synovium NP71/00	28467	26.06	6167.42	12334.84	RA Synovium	
RA Synovium NP45/00	28475	25.35	8888.66	17777.32	RA Synovium	
OA bone (biobank)	29217	30.23	729.87	729.87	OA bone (biobank)	
OA bone Sample 1	J. Emory	27.65	2743.38	5486.76	OA bone	
OA bone Sample 2	J. Emory	28.02	2258.96	4517.92	OA bone	
Cartilage (pool)	Normal	25.82	7006.64	14013.28	Cartilage (pool)	
Cartilage (pool)	OA	27.22	3408.61	6817.22	Cartilage (pool)	-2.06
PBL uninfected	28441	24.24	15680.49	31360.98	PBL uninfected	
PBL HIV IIIB	28442	25.43	8521.98	17043.96	PBL HIV IIIB	-1.84
MRC5 uninfected (100%)	29158	25.58	7922.19	15844.38	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	32.02	291.12	582.24	MRC5 HSV strain F	-27.21
W12 cells	29179	26.03	6269.24	12538.48	W12 cells	
Keratinocytes	29180	25.43	8538.15	17076.30	Keratinocytes	
B-actin control		29.74	938.61			
genomic		28.79	1522.16			
1.00E+05		20.84	100000			
1.00E+05		21.4	100000			

1.00E+04		24.5	10000			
1.00E+04		25.2	10000			
1.00E+03		28.45	1000			
1.00E+03		29.25	1000			
1.00E+02		35.34	100			
1.00E+02		33.61	100			
1.00E+01		38.95	10			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg1003328IG

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.13
colon tumor	1.59
colon tumor	-1.55
colon tumor	-1.65
lung tumor	-1.15
lung tumor	-1.34
lung tumor	-1.23
lung tumor	1.14
breast tumor	3.10
breast tumor	46.37
breast tumor	23.06
breast tumor	-1.23
brain stage 5 ALZ	-4.43
brain stage 5 ALZ	-1.06
brain stage 5 ALZ	-1.19
brain stage 5 ALZ	-1.74
lung 24	-17.21
lung 28	-18.70
lung 23	-8.96
asthmatic lung	-11.04
asthmatic lung	-1.22
asthmatic lung	2.66
asthmatic lung	1.02
endo VEGF	-1.23
endo bFGF	-2.24
heart T-1	-1.11
heart T-14	-1.27
heart T-3399	1.37
BM stim	2.10
osteo dif	3.42

Cartilage (pool)	-2.06
PBL HIV IIIB	-1.84
MRC5 HSV strain F	-27.21

Gene Name sbg1020829SGLT

5 Low overall expression in normal and disease samples. Highest normal expression in the whole brain, kidney, and thymus. Highest disease expression in the adenoid, tonsil, T cells, B cells, and eosinophils. Highly immune cell specific. Downregulation in 1 of 4 lung tumor samples and upregulation in 1 of 4 breast tumor samples indicates involvement in cancers of the lung and breast. Upregulation in 3 of 4 AD brain samples suggests an involvement in Alzheimer's disease.

10 Downregulation in 3 of 3 COPD samples implies a role in chronic obstructive pulmonary disease. Downregulation in the stimulated bone marrow sample. Upregulation in the differentiated osteoblast sample. Upregulation in the HSV-infected MRC5 cells suggests that this gene may be a host factor in HSV. Moderate to high expression in the OA and RA samples indicates a potential role in osteoarthritis and rheumatoid arthritis.

Sample sbg1020829SGLT	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	37.07, 40	7.33	0	3.67	3.06	16.34	59.89
Subcutaneous Adipose Zenbio	40, 40	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	32.13, 32.38	138.5	119.48	128.99	7.24	6.91	890.81
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	40, 40	0	0	0.00	2.17	23.04	0.00
Cervix	36.13, 40	12.82	0	6.41	2.42	20.66	132.44
Colon	36.93, 36.84	7.97	8.41	8.19	2.71	18.45	151.11
Endometrium	37.45, 37.41	5.84	5.98	5.91	0.73	68.21	403.14
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	36.53, 35.17	10.09	22.67	16.38	2.58	19.38	317.44
Jejunum	40, 35.73	0	16.2	8.10	6.60	7.58	61.36
Kidney	31.93, 31.01	155.27	269.39	212.33	2.12	23.58	5007.78
Liver	36.1, 35.88	13.05	14.82	13.94	1.50	33.33	464.50
Fetal Liver Clontech	35.06, 34.36	24.26	36.78	30.52	10.40	4.81	146.73
Lung	37.24, 40	6.63	0	3.32	2.57	19.46	64.49
Mammary Gland Clontech	34.25, 34.21	39.27	40.17	39.72	13.00	3.85	152.77
Myometrium	38.48, 35.31	3.16	20.87	12.02	2.34	21.37	256.73
Omentum	40, 38.91	0	2.45	1.23	3.94	12.69	15.55
Ovary	37.87, 37.06	4.56	7.37	5.97	4.34	11.52	68.72
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00

Parotid Gland	36.06, 37.07	13.32	7.31	10.32	5.48	9.12	94.11
Placenta Clontech	35.98, 38.73	13.96	2.72	8.34	5.26	9.51	79.28
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 40	0	0	0.00	1.23	40.65	0.00
Salivary Gland Clontech	37.05, 37.06	7.4	7.36	7.38	7.31	6.84	50.48
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	35.62, 35.72	17.34	16.35	16.85	4.92	10.16	171.19
Stomach	40, 40	0	1.61	0.81	2.73	18.32	14.74
Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	31.3, 31.09	226.24	257.15	241.70	9.89	5.06	1221.92
Thyroid	40, 40	0	0	0.00	2.77	18.05	0.00
Trachea Clontech	36.6, 36.64	9.68	9.44	9.56	9.71	5.15	49.23
Urinary Bladder	40, 40	0	0	0.00	5.47	9.14	0.00
Uterus	34.64, 36.65	31.06	9.41	20.24	5.34	9.36	189.47
genomic	29.07	853.08					
b-actin	27.08	2793.5					
1.00E+05	20.85	100000					
1.00E+05	21.11	100000					
1.00E+04	24.81	10000					
1.00E+04	24.95	10000					
1.00E+03	28.39	1000					
1.00E+03	28.9	1000					
1.00E+02	34.1	100					
1.00E+02	32.86	100					
1.00E+01	35.52	10					
1.00E+01	40	0					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg1020829SGLT	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detected/ 50 ng total RNA	Sample	Fold Change in Disease Populat ion
colon normal GW98-167	21941	31.06	206.55	413.10	colon normal	
colon tumor GW98-166	21940	31.18	193.59	387.18	colon tumor	-1.07
colon normal GW98-178	22080	30.74	244.37	488.74	colon normal	
colon tumor GW98-177	22060	30.37	299.28	598.56	colon tumor	1.22
colon normal GW98-561	23514	29.31	527.04	1054.08	colon normal	
colon tumor GW98-560	23513	31.86	134.48	268.96	colon tumor	-3.92

colon normal GW98-894	24691	31.84	135.33	270.66	colon normal	
colon tumor GW98-893	24690	31.9	131.57	263.14	colon tumor	-1.03
lung normal GW98-3	20742	28.81	689.14	1378.28	lung normal	
lung tumor GW98-2	20741	31.91	130.71	261.42	lung tumor	-5.27
lung normal GW97-179	20677	30.04	356.26	712.52	lung normal	
lung tumor GW97-178	20676	29.05	605.73	1211.46	lung tumor	1.70
lung normal GW98-165	21922	28.42	852.41	1704.82	lung normal	
lung tumor GW98-164	21921	30.51	277.13	554.26	lung tumor	-3.08
lung normal GW98-282	22584	31.23	188.34	376.68	lung normal	
lung tumor GW98-281	22583	30.46	285	570.00	lung tumor	1.51
breast normal GW00-392	28750	31.14	197.15	197.15	breast normal	
breast tumor GW00-391	28746	32.15	114.65	229.30	breast tumor	1.16
breast normal GW00-413	28798	34.87	26.64	26.64	breast normal	
breast tumor GW00-412	28797	31.83	136.42	272.84	breast tumor	10.24
breast normal GW00-235:238	27592-95	36.34	12.09	12.09	breast normal	
breast tumor GW00-231:234	27588-91	33.48	56.11	56.11	breast tumor	4.64
breast normal GW98-621	23656	32.39	100.78	201.56	breast normal	
breast tumor GW98-620	23655	31.4	171.82	343.64	breast tumor	1.70
brain normal BB99-542	25507	34.49	32.75	65.50	brain normal	
brain normal BB99-406	25509	34.01	42.2	84.40	brain normal	
brain normal BB99-904	25546	36.17	13.3	26.60	brain normal	
brain stage 5 ALZ BB99-874	25502	31.16	195.23	390.46	brain stage 5 ALZ	6.64
brain stage 5 ALZ BB99-887	25503	31.56	157.33	314.66	brain stage 5 ALZ	5.35
brain stage 5 ALZ BB99-862	25504	32.62	89.2	178.40	brain stage 5 ALZ	3.03
brain stage 5 ALZ BB99-927	25542	33.26	63.43	126.86	brain stage 5 ALZ	2.16
CT lung KC	normal	30.82	234.88	469.76	CT lung	
lung 26 KC	normal	30.21	325.42	325.42	lung 26	
lung 27 KC	normal	36.89	9	9.00	lung 27	
lung 24 KC	COPD	36.17	13.24	13.24	lung 24	-15.84
lung 28 KC	COPD	38.38	4.06	4.06	lung 28	-51.66
lung 23 KC	COPD	35.53	18.67	18.67	lung 23	-11.23
lung 25 KC	normal	34.37	34.83	34.83	lung 25	
asthmatic lung ODO3112	29321	33.65	51.41	51.41	asthmatic lung	-4.08
asthmatic lung ODO3433	29323	30.62	260.95	521.90	asthmatic lung	2.49
asthmatic lung ODO3397	29322	31.31	180.14	360.28	asthmatic lung	1.72
asthmatic lung ODO4928	29325	31.14	197.09	394.18	asthmatic lung	1.88
endo cells KC	control	32.56	92.23	92.23	endo cells	
endo VEGF KC		33.29	62.39	62.39	endo VEGF	-1.48
endo bFGF KC		32.55	92.65	92.65	endo bFGF	1.00
heart Clontech	normal	33.17	66.25	132.50	heart	
heart (T-1) ischemic	29417	33.07	70.16	140.32	heart T-1	1.06
heart (T-14) non-obstructive DCM	29422	34.64	30.13	60.26	heart T-14	-2.20
heart (T-3399) DCM	29426	32.53	93.63	187.26	heart T-3399	1.41

adenoid GW99-269	26162	28.92	650.55	1301.10	adenoid	
tonsil GW98-280	22582	27.11	1719.42	3438.84	tonsil	
T cells PC00314	28453	28.05	1037.04	2074.08	T cells	
PBMNC		36.57	10.71	10.71	PBMNC	
monocyte		33.22	64.68	129.36	monocyte	
B cells PC00665	28455	27.07	1757.79	3515.58	B cells	
dendritic cells 28441		33.77	48.05	96.10	dendritic cells	
neutrophils	28440	30.71	248.56	248.56	neutrophils	
eosinophils	28446	27.3	1549.7	3099.40	eosinophils	
BM unstim		30.06	352.26	352.26	BM unstim	
BM stim		34.14	39.39	39.39	BM stim	-8.94
osteo dif		36.29	12.42	12.42	osteo dif	12.42
osteo undif		40	0	0.00	osteo undif	
chondrocytes		32.11	117.39	293.48	chondrocytes	
OA Synovium IP12/01	29462	30.17	331.7	331.70	OA Synovium	
OA Synovium NP10/01	29461	32.05	120.98	241.96	OA Synovium	
OA Synovium NP57/00	28464	30.13	339.03	678.06	OA Synovium	
RA Synovium NP03/01	28466	31.28	182.96	365.92	RA Synovium	
RA Synovium NP71/00	28467	29.81	402.34	804.68	RA Synovium	
RA Synovium NP45/00	28475	30.22	324.14	648.28	RA Synovium	
OA bone (biobank)	29217	28.45	837.78	837.78	OA bone (biobank)	
OA bone Sample 1	J. Emory	30.21	325.03	650.06	OA bone	
OA bone Sample 2	J. Emory	29.8	406	812.00	OA bone	
Cartilage (pool)	Normal	31.09	203.28	406.56	Cartilage (pool)	
Cartilage (pool)	OA	32.18	112.77	225.54	Cartilage (pool)	-1.80
PBL uninfected	28441	29.17	567.22	1134.44	PBL uninfected	
PBL HIV IIIB	28442	30.73	246.69	493.38	PBL HIV IIIB	-2.30
MRC5 uninfected (100%)	29158	35.54	18.61	37.22	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	30.54	272.3	544.60	MRC5 HSV strain F	14.63
W12 cells	29179	32.28	107.25	214.50	W12 cells	
Keratinocytes	29180	34.27	36.84	73.68	Keratinocytes	
B-actin control		27.03	1793.92			
genomic		27.77	1204.8			
1.00E+05		19.84	100000			
1.00E+05		19.86	100000			
1.00E+04		23.46	10000			
1.00E+04		23.8	10000			
1.00E+03		27.45	1000			
1.00E+03		27.94	1000			
1.00E+02		33.86	100			
1.00E+02		31.41	100			
1.00E+01		40	0			
1.00E+01		36.88	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg1020829SGLT

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.07
colon tumor	1.22
colon tumor	-3.92
colon tumor	-1.03
lung tumor	-5.27
lung tumor	1.70
lung tumor	-3.08
lung tumor	1.51
breast tumor	1.16
breast tumor	10.24
breast tumor	4.64
breast tumor	1.70
brain stage 5 ALZ	6.64
brain stage 5 ALZ	5.35
brain stage 5 ALZ	3.03
brain stage 5 ALZ	2.16
lung 24	-15.84
lung 28	-51.66
lung 23	-11.23
asthmatic lung	-4.08
asthmatic lung	2.49
asthmatic lung	1.72
asthmatic lung	1.88
endo VEGF	-1.48
endo bFGF	1.00
heart T-1	1.06
heart T-14	-2.20
heart T-3399	1.41
BM stim	-8.94
osteo dif	12.42
Cartilage (pool)	-1.80
PBL HIV IIB	-2.30
MRC5 HSV strain F	14.63

5 Gene Name sbg1005450UDPGT

Low to moderate overall expression. Highest normal expression in endometrium, esophagus, and spleen with lower levels of expression in cerebellum, hypothalamus, rectum, and uterus. Highest disease expression in one of the OA synovium samples. Downregulation in 1 of 4 colon tumor samples is sufficient to make a disease claim in cancer of the colon. Upregulation in 1 of 4 lung tumor samples indicates a potential role for this gene in cancer of the lung. Downregulation in 2 of 4 AD brain samples suggests an involvement in Alzheimer's disease. Downregulation in 3 of 3 COPD lung samples and 4 of 4 asthmatic lung samples suggests involvement in chronic obstructive

pulmonary disease and asthma. Upregulation in the HSV-infected MRC5 cells suggests that this gene may be a host factor in HSV. Moderate expression in the B cells and the dendritic cells.

Sample sbg1005450UDPGT	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Averag e GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 40	0.15	0.17	0.16	3.06	16.34	2.61
Subcutaneous Adipose Zenbio	40, 40	0	0	0.00	0.96	52.36	0.00
Adrenal Gland Clontech	40, 40	0	0.14	0.07	0.61	81.97	5.74
Whole Brain Clontech	33.74, 40	12.07	0	6.04	7.24	6.91	41.68
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	32.07, 33.2	32.85	16.64	24.75	2.17	23.04	570.16
Cervix	40, 40	0	0	0.00	2.42	20.66	0.00
Colon	40, 35.16	0	5.12	2.56	2.71	18.45	47.23
Endometrium	32.73, 31.85	22.19	37.5	29.85	0.73	68.21	2035.81
Esophagus	32.67, 29.39	22.91	165.34	94.13	1.37	36.50	3435.22
Heart Clontech	37.12, 35.03	1.58	5.55	3.57	1.32	37.88	135.04
Hypothalamus	34.08, 40	9.84	0	4.92	0.32	155.28	763.98
Ileum	34.35	8.33		8.33	2.58	19.38	161.43
Jejunum	40, 40	0	0	0.00	6.60	7.58	0.00
Kidney	38.89, 40	0.54	0	0.27	2.12	23.58	6.37
Liver	36.32, 40	2.55	0	1.28	1.50	33.33	42.50
Fetal Liver Clontech	36.96	1.74		1.74	10.40	4.81	8.37
Lung	40, 40	0	0	0.00	2.57	19.46	0.00
Mammary Gland Clontech	40, 40	0	0	0.00	13.00	3.85	0.00
Myometrium	40, 38.22	0	0.82	0.41	2.34	21.37	8.76
Omentum	36.17, 40	2.8	0	1.40	3.94	12.69	17.77
Ovary	40, 40	0	0	0.00	4.34	11.52	0.00
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 38.35	0	0.75	0.38	1.57	31.85	11.94
Parotid Gland	40, 40	0	0	0.00	5.48	9.12	0.00
Placenta Clontech	39.06, 35.49	0.49	4.22	2.36	5.26	9.51	22.39
Prostate	38.81, 40	0.57	0	0.29	3.00	16.67	4.75
Rectum	35.22, 33.25	4.94	16.2	10.57	1.23	40.65	429.67
Salivary Gland Clontech	32.56, 34.56	24.55	7.36	15.96	7.31	6.84	109.13
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	34.26, 40	8.8	0	4.40	1.21	41.32	181.82
Small Intestine Clontech	40	0	6.23	3.12	0.98	51.07	159.09
Spleen	40, 27.36	0	560.92	280.46	4.92	10.16	2850.20
Stomach	33.49, 39.12	13.98	0.47	7.23	2.73	18.32	132.33

Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	40, 35.33	0	4.64	2.32	9.89	5.06	11.73
Thyroid	37.18, 35.52	1.53	4.13	2.83	2.77	18.05	51.08
Trachea Clontech	40, 40	0	0	0.00	9.71	5.15	0.00
Urinary Bladder	40, 40	0	0.16	0.08	5.47	9.14	0.73
Uterus	30.11	106.94	0	53.47	5.34	9.36	500.66
genomic	35.81	3.47					
b-actin	26.86	757.01					
1.00E+05	18.99	100000					
1.00E+05	19.13	100000					
1.00E+04	22.43	10000					
1.00E+04	22.31	10000					
1.00E+03	25.74	1000					
1.00E+03	25.99	1000					
1.00E+02	31.47	100					
1.00E+02	29.82	100					
1.00E+01	40	0					
1.00E+01	40	0					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	26.02	-1					
NTC	40	0					

Sample sbg1005450UDPGT	Reg number (GSK identifie r)	Ct	Mean GOI copies	copies of mRNA detecte d/50 ng total RNA	Sample	Fold Change in Disease Populati on
colon normal GW98-167	21941	40	0.17	0.34	colon normal	
colon tumor GW98-166	21940	39.88	0.29	0.58	colon tumor	1.71
colon normal GW98-178	22080	40	0	0.00	colon normal	
colon tumor GW98-177	22060	40	0	0.00	colon tumor	0.00
colon normal GW98-561	23514	40	0	0.00	colon normal	
colon tumor GW98-560	23513	40	0	0.00	colon tumor	0.00
colon normal GW98-894	24691	33.84	10.47	20.94	colon normal	
colon tumor GW98-893	24690	40	0	0.00	colon tumor	-20.94
lung normal GW98-3	20742	40	0	0.00	lung normal	
lung tumor GW98-2	20741	40	0	0.00	lung tumor	0.00
lung normal GW97-179	20677	31.67	37.94	75.88	lung normal	
lung tumor GW97-178	20676	33.08	16.47	32.94	lung tumor	-2.30
lung normal GW98-165	21922	40	0	0.00	lung normal	
lung tumor GW98-164	21921	40	0	0.00	lung tumor	0.00
lung normal GW98-282	22584	40	0	0.00	lung normal	
lung tumor GW98-281	22583	35.03	5.16	10.32	lung tumor	10.32
breast normal GW00-392	28750	32.64	21.38	21.38	breast normal	

breast tumor GW00-391	28746	31.67	37.98	75.96	breast tumor	3.55
breast normal GW00-413	28798	32.54	22.63	22.63	breast normal	
breast tumor GW00-412	28797	29.23	161.71	323.42	breast tumor	14.29
breast normal GW00-235:238	27592-95	37.05	1.55	1.55	breast normal	
breast tumor GW00-231:234	27588-91	35.03	5.17	5.17	breast tumor	3.34
breast normal GW98-621	23656	34.12	8.87	17.74	breast normal	
breast tumor GW98-620	23655	40	0	0.00	breast tumor	-17.74
brain normal BB99-542	25507	34.28	8.05	16.10	brain normal	
brain normal BB99-406	25509	40	0	0.00	brain normal	
brain normal BB99-904	25546	40	0	0.00	brain normal	
brain stage 5 ALZ BB99-874	25502	38.8	0.55	1.10	brain stage 5 ALZ	-4.88
brain stage 5 ALZ BB99-887	25503	40	0	0.00	brain stage 5 ALZ	-5.37
brain stage 5 ALZ BB99-862	25504	36.16	2.64	5.28	brain stage 5 ALZ	-1.02
brain stage 5 ALZ BB99-927	25542	40	0	0.00	brain stage 5 ALZ	-5.37
CT lung KC	normal	36.61	2.02	4.04	CT lung	
lung 26 KC	normal				lung 26	
lung 27 KC	normal	40	0	0.00	lung 27	
lung 24 KC	COPD	40	0	0.00	lung 24	-1.35
lung 28 KC	COPD	40	0	0.00	lung 28	-1.35
lung 23 KC	COPD	40	0	0.00	lung 23	-1.35
lung 25 KC	normal	40	0	0.00	lung 25	
asthmatic lung ODO3112	29321	38.19	0.79	0.79	asthmatic lung	-1.70
asthmatic lung ODO3433	29323	36.09	2.76	5.52	asthmatic lung	4.10
asthmatic lung ODO3397	29322	40	0	0.00	asthmatic lung	-1.35
asthmatic lung ODO4928	29325	40	0	0.00	asthmatic lung	-1.35
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		40	0	0.00	endo bFGF	0.00
heart Clontech	normal	40	0	0.00	heart	
heart (T-1) ischemic	29417	38.36	0.71	1.42	heart T-1	1.42
heart (T-14) non-obstructive DCM	29422	40	0	0.00	heart T-14	0.00
heart (T-3399) DCM	29426	40	0	0.00	heart T-3399	0.00
adenoid GW99-269	26162	38.96	0.5	1.00	adenoid	
tonsil GW98-280	22582	35.44	4.04	8.08	tonsil	
T cells PC00314	28453	38.83	0.54	1.08	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		35.1	4.94	9.88	monocyte	
B cells PC00665	28455	33.32	14.31	28.62	B cells	
dendritic cells 28441		32.53	22.85	45.70	dendritic cells	
neutrophils	28440	34.43	7.39	7.39	neutrophils	
eosinophils	28446	40	0	0.00	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim		34.12	8.87	8.87	BM stim	8.87

osteo dif		40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		34.51	7.05	17.63	chondrocytes	
OA Synovium IP12/01	29462	40	0	0.00	OA Synovium	
OA Synovium NP10/01	29461	27.21	538.51	1077.02	OA Synovium	
OA Synovium NP57/00	28464	33.5	12.85	25.70	OA Synovium	
RA Synovium NP03/01	28466	39.09	0.46	0.92	RA Synovium	
RA Synovium NP71/00	28467	40	0	0.00	RA Synovium	
RA Synovium NP45/00	28475	40	0	0.00	RA Synovium	
OA bone (biobank)	29217	40	0	0.00	OA bone (biobank)	
OA bone Sample 1	J. Emory	35.23	4.59	9.18	OA bone	
OA bone Sample 2	J. Emory	37.1	1.51	3.02	OA bone	
Cartilage (pool)	Normal	35.45	4.01	8.02	Cartilage (pool)	
Cartilage (pool)	OA	40	0	0.00	Cartilage (pool)	-8.02
PBL uninfected	28441	40	0	0.00	PBL uninfected	
PBL HIV IIIB	28442	40	0	0.00	PBL HIV IIIB	0.00
MRC5 uninfected (100%)	29158	40	0.17	0.34	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	30.15	93.76	187.52	MRC5 HSV strain F	551.53
W12 cells	29179	40	0	0.00	W12 cells	
Keratinocytes	29180	35.72	3.44	6.88	Keratinocytes	
B-actin control		26.57	788.4			
genomic		25.69	1326.94			
1.00E+05		18.72	100000			
1.00E+05		18.74	100000			
1.00E+04		22.11	10000			
1.00E+04		22.15	10000			
1.00E+03		25.57	1000			
1.00E+03		25.54	1000			
1.00E+02		31.37	100			
1.00E+02		29.65	100			
1.00E+01		40	0			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg1005450UDPGT

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.71
colon tumor	0.00
colon tumor	0.00
colon tumor	-20.94

lung tumor	0.00
lung tumor	-2.30
lung tumor	0.00
lung tumor	10.32
breast tumor	3.55
breast tumor	14.29
breast tumor	3.34
breast tumor	-17.74
brain stage 5 ALZ	-4.88
brain stage 5 ALZ	-5.37
brain stage 5 ALZ	-1.02
brain stage 5 ALZ	-5.37
lung 24	-1.35
lung 28	-1.35
lung 23	-1.35
asthmatic lung	-1.70
asthmatic lung	4.10
asthmatic lung	-1.35
asthmatic lung	-1.35
endo VEGF	0.00
endo bFGF	0.00
heart T-1	1.42
heart T-14	0.00
heart T-3399	0.00
BM stim	8.87
osteo undif	0.00
Cartilage (pool)	-8.02
PBL HIV IIIB	0.00
MRC5 HSV strain F	551.53

Gene Name sbg1002620Tia

- 5 Moderate overall expression. Highest normal expression in the whole brain, endometrium, myometrium, placenta, and rectum. Highest disease expression in the one of the colon normal/tumor pairs, the normal lung samples, one of the asthmatic lung samples, the neutrophils, the eosinophils, and one of the RA synovium samples. Expressed at high levels in all of the samples representative of the GI tract indicating a potential role for this gene in IBS, IBD, and Crohn's
- 10 disease. Downregulation in 1 of 3 COPD lung samples suggests involvement in chronic obstructive pulmonary disease. Upregulation in 1 of 4 asthmatic lung samples implies a role in asthma. High expression in the OA synovium and bone samples as well as in the RA synovium samples. Also high expression in the chondrocytes. Variable expression in the immune cells with highest expression in the neutrophils and eosinophils and lowest expression in the dendritic cells.
- 15 Corroborating high expression in B and T cells as well as OA samples implicates this gene in osteoarthritis and rheumatoid arthritis.

Sample sbg1002620Tia	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18 S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA

Subcutaneous Adipocytes Zenbio	35.04, 34.4	201.66	274.43	238.05	3.06	16.34	3889.62
Subcutaneous Adipose Zenbio	38.03, 38.45	48.67	39.85	44.26	0.96	52.36	2317.28
Adrenal Gland Clontech	38.71, 38.14	35.25	46.23	40.74	0.61	81.97	3339.34
Whole Brain Clontech	29.27, 29.32	3152.23	3071.49	3111.86	7.24	6.91	21490.75
Fetal Brain Clontech	40, 37.57	0	60.7	30.35	0.48	103.95	3154.89
Cerebellum Clontech	39.37, 39.14	25.78	28.75	27.27	2.17	23.04	628.23
Cervix	34.05, 34.32	323.57	285.02	304.30	2.42	20.66	6287.09
Colon	32.64, 32.98	633.12	537.54	585.33	2.71	18.45	10799.45
Endometrium	34.44, 33.84	269.09	357.16	313.13	0.73	68.21	21359.14
Esophagus	35.48, 35.21	163.52	186.15	174.84	1.37	36.50	6380.84
Heart Clontech	38.67, 39.08	35.94	29.52	32.73	1.32	37.88	1239.77
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	33.07, 32.9	516.19	559.94	538.07	2.58	19.38	10427.62
Jejunum	30.58, 30.66	1688.39	1625.61	1657.00	6.60	7.58	12553.03
Kidney	34.9, 33.68	216.07	385.19	300.63	2.12	23.58	7090.33
Liver	37.17, 36.49	73.4	101.31	87.36	1.50	33.33	2911.83
Fetal Liver Clontech	33.99, 34.79	332.15	227.82	279.99	10.40	4.81	1346.08
Lung	34.67, 34.06	240.47	321.54	281.01	2.57	19.46	5467.02
Mammary Gland Clontech	29.3, 29.19	3098.36	3272.39	3185.38	13.00	3.85	12251.44
Myometrium	32.45, 31.79	692.54	946.75	819.65	2.34	21.37	17513.78
Omentum	32.88, 33.43	563.23	434.44	498.84	3.94	12.69	6330.39
Ovary	33.02, 32.92	528.43	553.26	540.85	4.34	11.52	6230.93
Pancreas	37.31, 39.81	68.49	20.84	44.67	0.81	61.80	2760.51
Head of Pancreas	38.5, 39.16	38.99	28.45	33.72	1.57	31.85	1073.89
Parotid Gland	34.48, 34.22	263.15	298.49	280.82	5.48	9.12	2562.23
Placenta Clontech	31.16, 30.91	1280.82	1442.99	1361.91	5.26	9.51	12945.87
Prostate	33.5, 33.11	420.13	506.76	463.45	3.00	16.67	7724.08
Rectum	34.48, 33.88	263.61	350.22	306.92	1.23	40.65	12476.22
Salivary Gland Clontech	34.48, 34.32	263.4	284.18	273.79	7.31	6.84	1872.71
Skeletal Muscle Clontech	40, 39.37	0	25.73	12.87	1.26	39.68	510.52
Skin	35.52, 35.13	160.58	193.62	177.10	1.21	41.32	7318.18
Small Intestine Clontech	36.79, 36.59	87.74	96.5	92.12	0.98	51.07	4704.80
Spleen	34.45, 34.51	267.45	260	263.73	4.92	10.16	2680.13
Stomach	35.16, 33.89	191.03	348.48	269.76	2.73	18.32	4940.57
Testis Clontech	38.19, 37.07	45.22	76.91	61.07	0.57	87.87	5365.99
Thymus Clontech	33.74, 33.57	374.59	406.79	390.69	9.89	5.06	1975.18
Thyroid	34.18, 33.46	304.38	427.57	365.98	2.77	18.05	6606.05
Trachea Clontech	32.67, 31.27	623.94	1213.65	918.80	9.71	5.15	4731.18
Urinary Bladder	32.07, 31.34	830.04	1176.15	1003.10	5.47	9.14	9169.06
Uterus	31.75, 31.37	968.5	1157.09	1062.80	5.34	9.36	9951.26
genomic	31.33	1181.44					
b-actin	28.56	4411.32					
1.00E+05	22.12	100000					

1.00E+05	22.12	100000					
1.00E+04	26.72	10000					
1.00E+04	26.91	10000					
1.00E+03	31.28	1000					
1.00E+03	31.5	1000					
1.00E+02	36.35	100					
1.00E+02	37.09	100					
1.00E+01	40	10					
1.00E+01	40	10					
1.00E-00	40	1					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg1002620T1a	Reg number (GSK identifie r)	Ct	Mean GOI copies	copies of mRNA detected/ 50 ng total RNA	Sample	Fold Change in Disease Populati on
colon normal GW98-167	21941	24.54	22693.01	45386.02	colon normal	
colon tumor GW98-166	21940	24.18	26862.61	53725.22	colon tumor	1.18
colon normal GW98-178	22080	27.08	6895.34	13790.68	colon normal	
colon tumor GW98-177	22060	28.41	3692.19	7384.38	colon tumor	-1.87
colon normal GW98-561	23514	26.58	8698.68	17397.36	colon normal	
colon tumor GW98-560	23513	27.85	4799.22	9598.44	colon tumor	-1.81
colon normal GW98-894	24691	25.9	11972.57	23945.14	colon normal	
colon tumor GW98-893	24690	28.04	4396.4	8792.80	colon tumor	-2.72
lung normal GW98-3	20742	24.25	26016.9	52033.80	lung normal	
lung tumor GW98-2	20741	27.64	5300.37	10600.74	lung tumor	-4.91
lung normal GW97-179	20677	25.1	17476.66	34953.32	lung normal	
lung tumor GW97-178	20676	25.53	14274.54	28549.08	lung tumor	-1.22
lung normal GW98-165	21922	24.62	21917.37	43834.74	lung normal	
lung tumor GW98-164	21921	25.64	13526.49	27052.98	lung tumor	-1.62
lung normal GW98-282	22584	27.08	6884.03	13768.06	lung normal	
lung tumor GW98-281	22583	25.37	15385.8	30771.60	lung tumor	2.23
breast normal GW00-392	28750	26.07	11065.25	11065.25	breast normal	
breast tumor GW00-391	28746	26.87	7611.48	15222.96	breast tumor	1.38
breast normal GW00-413	28798	28.65	3294.68	3294.68	breast normal	
breast tumor GW00-412	28797	28.52	3496.94	6993.88	breast tumor	2.12
breast normal GW00-235:238	27592-95	29.47	2243.69	2243.69	breast normal	
breast tumor GW00-231:234	27588-91	25.83	12385.23	12385.23	breast tumor	5.52
breast normal GW98-621	23656	26.05	11188.07	22376.14	breast normal	
breast tumor GW98-620	23655	26.03	11303.95	22607.90	breast tumor	1.01

brain normal BB99-542	25507	27.68	5198.79	10397.58	brain normal	
brain normal BB99-406	25509	29.81	1909.01	3818.02	brain normal	
brain normal BB99-904	25546	31.84	735.25	1470.50	brain normal	
brain stage 5 ALZ BB99-874	25502	28.43	3650.66	7301.32	brain stage 5 ALZ	1.40
brain stage 5 ALZ BB99-887	25503	29.01	2785.56	5571.12	brain stage 5 ALZ	1.07
brain stage 5 ALZ BB99-862	25504	29.65	2059.62	4119.24	brain stage 5 ALZ	-1.27
brain stage 5 ALZ BB99-927	25542	30.01	1742.3	3484.60	brain stage 5 ALZ	-1.50
CT lung KC	normal	25.49	14553.17	29106.34	CT lung	
lung 26 KC	normal	31.8	749.93	749.93	lung 26	
lung 27 KC	normal	33.35	362.66	362.66	lung 27	
lung 24 KC	COPD	30.67	1275.68	1275.68	lung 24	-6.03
lung 28 KC	COPD	29.25	2490.39	2490.39	lung 28	-3.09
lung 23 KC	COPD	30.11	1661.24	1661.24	lung 23	-4.63
lung 25 KC	normal	32.45	553.75	553.75	lung 25	
asthmatic lung ODO3112	29321	27.3	6215.19	6215.19	asthmatic lung	-1.24
asthmatic lung ODO3433	29323	26.66	8407.3	16814.60	asthmatic lung	2.19
asthmatic lung ODO3397	29322	24.06	28466.73	56933.46	asthmatic lung	7.40
asthmatic lung ODO4928	29325	26.22	10313.71	20627.42	asthmatic lung	2.68
endo cells KC	control	40	0	0.00	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	0.00
endo bFGF KC		40	0	0.00	endo bFGF	0.00
heart Clontech	normal	27.58	5449.78	10899.56	heart	
heart (T-1) ischemic	29417	28.42	3670.86	7341.72	heart T-1	-1.48
heart (T-14) non- obstructive DCM	29422	27.18	6570.11	13140.22	heart T-14	1.21
heart (T-3399) DCM	29426	26.23	10277.2	20554.40	heart T-3399	1.89
adenoid GW99-269	26162	31.98	688.86	1377.72	adenoid	
tonsil GW98-280	22582	29.31	2421.67	4843.34	tonsil	
T cells PC00314	28453	29.53	2178.21	4356.42	T cells	
PBMNC		33.23	383.88	383.88	PBMNC	
monocyte		31.07	1057.9	2115.80	monocyte	
B cells PC00665	28455	35.97	106.01	212.02	B cells	
dendritic cells 28441		33.56	328.62	657.24	dendritic cells	
neutrophils	28440	22.32	64510.36	64510.36	neutrophils	
eosinophils	28446	24.18	26910.17	53820.34	eosinophils	
BM unstim		30.35	1480.07	1480.07	BM unstim	
BM stim		31.71	782.56	782.56	BM stim	-1.89
osteo dif		31.42	895.71	895.71	osteo dif	2.03
osteo undif		32.93	440.66	440.66	osteo undif	
chondrocytes		28.98	2820.8	7052.00	chondrocytes	
OA Synovium IP12/01	29462	25.37	15383.84	15383.84	OA Synovium	
OA Synovium NP10/01	29461	27.12	6763.44	13526.88	OA Synovium	

OA Synovium NP57/00	28464	26.48	9130.81	18261.62	OA Synovium	
RA Synovium NP03/01	28466	27.78	4967.23	9934.46	RA Synovium	
RA Synovium NP71/00	28467	24.72	20923.66	41847.32	RA Synovium	
RA Synovium NP45/00	28475	26.15	10658.82	21317.64	RA Synovium	
OA bone (biobank)	29217	28.68	3248.19	3248.19	OA bone (biobank)	
OA bone Sample 1	J. Emory	27.19	6545.82	13091.64	OA bone	
OA bone Sample 2	J. Emory	27.24	6384.92	12769.84	OA bone	
Cartilage (pool)	Normal	26.28	10016.65	20033.30	Cartilage (pool)	
Cartilage (pool)	OA	26.67	8342.92	16685.84	Cartilage (pool)	-1.20
PBL uninfected	28441	31.05	1069.84	2139.68	PBL uninfected	
PBL HIV IIIB	28442	31.7	788.06	1576.12	PBL HIV IIIB	-1.36
MRC5 uninfected (100%)	29158	26.37	9631.13	19262.26	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	28.38	3747.38	7494.76	MRC5 HSV strain F	-2.57
W12 cells	29179	35.15	155.25	310.50	W12 cells	
Keratinocytes	29180	34.93	172.87	345.74	Keratinocytes	
B-actin control		28.06	4342.74			
genomic		30.54	1356.79			
1.00E+05		21.39	100000			
1.00E+05		21.64	100000			
1.00E+04		26.21	10000			
1.00E+04		26.24	10000			
1.00E+03		30.9	1000			
1.00E+03		30.97	1000			
1.00E+02		36.34	100			
1.00E+02		36.22	100			
1.00E+01		40	10			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg1002620T1a

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Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.18
colon tumor	-1.87
colon tumor	-1.81
colon tumor	-2.72
lung tumor	-4.91
lung tumor	-1.22
lung tumor	-1.62
lung tumor	2.23
breast tumor	1.38

breast tumor	2.12
breast tumor	5.52
breast tumor	1.01
brain stage 5 ALZ	1.40
brain stage 5 ALZ	1.07
brain stage 5 ALZ	-1.27
brain stage 5 ALZ	-1.50
lung 24	-6.03
lung 28	-3.09
lung 23	-4.63
asthmatic lung	-1.24
asthmatic lung	2.19
asthmatic lung	7.40
asthmatic lung	2.68
endo VEGF	0.00
endo bFGF	0.00
heart T-1	-1.48
heart T-14	1.21
heart T-3399	1.89
BM stim	-1.89
osteo dif	2.03
Cartilage (pool)	-1.20
PBL HIV IIIB	-1.36
MRC5 HSV strain F	-2.57

Gene Name sbg1002620Ttb

- 5 Moderate to high overall expression. Highest normal expression in whole brain, endometrium, jejunum, placenta, thymus, and urinary bladder. Highest disease expression in one of the colon normal/tumor pairs, one of the normal lung samples, one of the asthmatic lung samples, the neutrophils, and the eosinophils. Strong expression in all of the GI tract samples implicates this gene in IBS, IBD, and Crohn's disease. Downregulation in 1 of 4 lung tumor samples is sufficient to make a disease claim in cancer of the lung. Downregulation in 3 of 3 COPD lung samples suggests involvement in chronic obstructive pulmonary disease. Upregulation in 1 of 4 asthmatic lung samples implies a role in asthma. Upregulation in 2 of 3 heart samples suggests this gene may play a role in non-obstructive and obstructive dilated cardiac myopathy. High expression in the RA and OA synovium samples as well as high expression in the chondrocytes and T cells implicates this gene in osteoarthritis and rheumatoid arthritis.
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- 15

Sample sbg1002620Ttb	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Averag e GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected /50 ng total RNA
Subcutaneous Adipocytes Zenbio	31.35, 31.44	58.54	55.11	56.83	3.06	16.34	928.51
Subcutaneous Adipose Zenbio	35.12, 34.21	5	9.05	7.03	0.96	52.36	367.80
Adrenal Gland Clontech	40, 34.29	0	8.61	4.31	0.61	81.97	352.87
Whole Brain Clontech	26.02, 26.06	1897.9	1849.19	1873.55	7.24	6.91	12938.85

Fetal Brain Clontech	40, 36.43	0	2.13	1.07	0.48	103.95	110.71
Cerebellum Clontech	40, 36.05	0	2.74	1.37	2.17	23.04	31.57
Cervix	32.23, 33.04	33.11	19.47	26.29	2.42	20.66	543.18
Colon	30.44, 30.45	105.93	105.29	105.61	2.71	18.45	1948.52
Endometrium	30.86, 30.56	80.75	97.92	89.34	0.73	68.21	6093.79
Esophagus	33.03, 32.34	19.62	30.66	25.14	1.37	36.50	917.52
Heart Clontech	40, 35.05	0	5.26	2.63	1.32	37.88	99.62
Hypothalamus	40, 36.17	0	2.53	1.27	0.32	155.28	196.43
Ileum	31.25, 30.31	62.52	115.58	89.05	2.58	19.38	1725.78
Jejunum	27.75, 27.93	612.01	543.46	577.74	6.60	7.58	4376.78
Kidney	32.59, 31.86	26.03	42.14	34.09	2.12	23.58	803.89
Liver	34.66, 34.5	6.77	7.52	7.15	1.50	33.33	238.17
Fetal Liver Clontech	29.08, 28.58	256.83	356.67	306.75	10.40	4.81	1474.76
Lung	30.74, 30.68	87.44	90.91	89.18	2.57	19.46	1734.92
Mammary Gland Clontech	27.49, 26.81	725.02	1132.42	928.72	13.00	3.85	3572.00
Myometrium	31.2, 30.29	64.54	117.26	90.90	2.34	21.37	1942.31
Omentum	31.19, 30.12	65.05	130.86	97.96	3.94	12.69	1243.08
Ovary	30.24, 30.54	120.95	99.3	110.13	4.34	11.52	1268.72
Pancreas	36.01, 36.55	2.81	1.97	2.39	0.81	61.80	147.71
Head of Pancreas	33.95, 35.73	10.72	3.36	7.04	1.57	31.85	224.20
Parotid Gland	32.16, 33.16	34.51	18.05	26.28	5.48	9.12	239.78
Placenta Clontech	28.42, 28.02	395.01	512.77	453.89	5.26	9.51	4314.54
Prostate	30.61, 31.28	95.23	61.5	78.37	3.00	16.67	1306.08
Rectum	30.5, 30.93	101.73	76.9	89.32	1.23	40.65	3630.69
Salivary Gland Clontech	31.17, 31.07	65.95	70.23	68.09	7.31	6.84	465.73
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	34.37, 33.12	8.18	18.53	13.36	1.21	41.32	551.86
Small Intestine Clontech	36.71, 34.96	1.78	5.55	3.67	0.98	51.07	187.18
Spleen	30.54, 31.29	99.47	60.88	80.18	4.92	10.16	814.79
Stomach	32.4, 31.53	29.49	52	40.75	2.73	18.32	746.25
Testis Clontech	34.4, 35.19	8.03	4.79	6.41	0.57	87.87	563.27
Thymus Clontech	27.18, 27.12	888.84	924.29	906.57	9.89	5.06	4583.24
Thyroid	32.17, 30.89	34.36	79.27	56.82	2.77	18.05	1025.54
Trachea Clontech	30.01, 29.25	140.31	230.28	185.30	9.71	5.15	954.15
Urinary Bladder	28.33, 27.87	420.47	565.71	493.09	5.47	9.14	4507.22
Uterus	29.09, 28.81	255.27	308	281.64	5.34	9.36	2637.03
genomic	27.16	900.78					
b-actin	27.4	769.87					
1.00E+05	19.87	100000					
1.00E+05	19.95	100000					
1.00E+04	23.4	10000					
1.00E+04	23.39	10000					
1.00E+03	26.94	1000					
1.00E+03	26.95	1000					
1.00E+02	31.02	100					

1.00E+02	30.96	100					
1.00E+01	33.46	10					
1.00E+01	40	0					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg1002620T1b	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detected /50 ng total RNA	Sample	Fold Chang e in Diseas e Popula tion
colon normal GW98-167	21941	22.85	18631.2	37262.40	colon normal	
colon tumor GW98-166	21940	22.51	23090.96	46181.92	colon tumor	1.24
colon normal GW98-178	22080	25.49	3620.45	7240.90	colon normal	
colon tumor GW98-177	22060	26.88	1527.3	3054.60	colon tumor	-2.37
colon normal GW98-561	23514	25.37	3901.36	7802.72	colon normal	
colon tumor GW98-560	23513	26.08	2512.21	5024.42	colon tumor	-1.55
colon normal GW98-894	24691	23.78	10441.49	20882.98	colon normal	
colon tumor GW98-893	24690	25.54	3515.48	7030.96	colon tumor	-2.97
lung normal GW98-3	20742	22.6	21810.56	43621.12	lung normal	
lung tumor GW98-2	20741	26.19	2349.32	4698.64	lung tumor	-9.28
lung normal GW97-179	20677	23.38	13423.28	26846.56	lung normal	
lung tumor GW97-178	20676	24.51	6653.03	13306.06	lung tumor	-2.02
lung normal GW98-165	21922	23.68	11120.91	22241.82	lung normal	
lung tumor GW98-164	21921	24.37	7242.32	14484.64	lung tumor	-1.54
lung normal GW98-282	22584	25.05	4745.83	9491.66	lung normal	
lung tumor GW98-281	22583	23.57	11943.28	23886.56	lung tumor	2.52
breast normal GW00-392	28750	24.84	5415.88	5415.88	breast normal	
breast tumor GW00-391	28746	24.98	4973.9	9947.80	breast tumor	1.84
breast normal GW00-413	28798	24.69	5954.77	5954.77	breast normal	
breast tumor GW00-412	28797	26.38	2081.99	4163.98	breast tumor	-1.43
breast normal GW00-235:238	27592-95	25.04	4792.18	4792.18	breast normal	
breast tumor GW00-231:234	27588-91	23.63	11520.86	11520.86	breast tumor	2.40
breast normal GW98-621	23656	23.22	14836.24	29672.48	breast normal	
breast tumor GW98-620	23655	24.24	7879	15758.00	breast tumor	-1.88
brain normal BB99-542	25507	25.16	4447.15	8894.30	brain normal	
brain normal BB99-406	25509	27.05	1377.71	2755.42	brain normal	
brain normal BB99-904	25546	29.35	330.53	661.06	brain normal	
brain stage 5 ALZ BB99-874	25502	27.64	956.16	1912.32	brain stage 5 ALZ	-2.15
brain stage 5 ALZ	25503	27.02	1400.04	2800.08	brain stage 5	-1.47

BB99-887					ALZ	
brain stage 5 ALZ BB99-862	25504	27.4	1105.21	2210.42	brain stage 5 ALZ	-1.86
brain stage 5 ALZ BB99-927	25542	27.1	1336.02	2672.04	brain stage 5 ALZ	-1.54
CT lung KC	normal	23.52	12295.29	24590.58	CT lung	
lung 26 KC	normal	31.42	91.19	91.19	lung 26	
lung 27 KC	normal	32.34	51.71	51.71	lung 27	
lung 24 KC	COPD	31.27	100.29	100.29	lung 24	-61.80
lung 28 KC	COPD	28.64	511.37	511.37	lung 28	-12.12
lung 23 KC	COPD	30.52	159.17	159.17	lung 23	-38.94
lung 25 KC	normal	32.15	57.91	57.91	lung 25	
asthmatic lung ODO3112	29321	23.19	15086.65	15086.65	asthmatic lung	2.43
asthmatic lung ODO3433	29323	24.76	5706.9	11413.80	asthmatic lung	1.84
asthmatic lung ODO3397	29322	21.71	37760.01	75520.02	asthmatic lung	12.18
asthmatic lung ODO4928	29325	24.16	8255.16	16510.32	asthmatic lung	2.66
endo cells KC	control	37.31	2.36	2.36	endo cells	
endo VEGF KC		40	0	0.00	endo VEGF	-2.36
endo bFGF KC		35.67	6.54	6.54	endo bFGF	2.77
heart Clontech	normal	26.32	2170.24	4340.48	heart	
heart (T-1) ischemic	29417	25.87	2863.04	5726.08	heart T-1	1.32
heart (T-14) non- obstructive DCM	29422	24.62	6200.03	12400.06	heart T-14	2.86
heart (T-3399) DCM	29426	24.06	8775.18	17550.36	heart T-3399	4.04
adenoid GW99-269	26162	29.2	362.88	725.76	adenoid	
tonsil GW98-280	22582	27.24	1222.33	2444.66	tonsil	
T cells PC00314	28453	28.09	723.06	1446.12	T cells	
PBMNC		30.67	145.75	145.75	PBMNC	
monocyte		28.42	587.16	1174.32	monocyte	
B cells PC00665	28455	34.17	16.57	33.14	B cells	
dendritic cells 28441		31.78	72.95	145.90	dendritic cells	
neutrophils	28440	21.46	44297.23	44297.23	neutrophils	
eosinophils	28446	22.79	19332.21	38664.42	eosinophils	
BM unstim		29.22	358.53	358.53	BM unstim	
BM stim		31.27	100.39	100.39	BM stim	-3.57
osteo dif		30.14	202.25	202.25	osteo dif	4.97
osteo undif		32.72	40.67	40.67	osteo undif	
chondrocytes		27.3	1178.3	2945.75	chondrocytes	
OA Synovium IP12/01	29462	23.33	13860.23	13860.23	OA Synovium	
OA Synovium NP10/01	29461	25.3	4080.49	8160.98	OA Synovium	
OA Synovium NP57/00	28464	25.23	4253.8	8507.60	OA Synovium	
RA Synovium NP03/01	28466	25.46	3686.62	7373.24	RA Synovium	
RA Synovium NP71/00	28467	23.31	14036.44	28072.88	RA Synovium	
RA Synovium NP45/00	28475	24.28	7658.52	15317.04	RA Synovium	
OA bone (biobank)	29217	26.48	1958.1	1958.10	OA bone (biobank)	

OA bone Sample 1	J. Emory	25.28	4131.76	8263.52	OA bone	
OA bone Sample 2	J. Emory	25.23	4242.9	8485.80	OA bone	
Cartilage (pool)	Normal	24.05	8829.67	17659.34	Cartilage (pool)	
Cartilage (pool)	OA	24.28	7685.44	15370.88	Cartilage (pool)	-1.15
PBL uninfected	28441	29.33	334.71	669.42	PBL uninfected	
PBL HIV IIIB	28442	29.59	283.96	567.92	PBL HIV IIIB	-1.18
MRC5 uninfected (100%)	29158	23.92	9595.12	19190.24	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	25.2	4341.36	8682.72	MRC5 HSV strain F	-2.21
W12 cells	29179	30.43	168.9	337.80	W12 cells	
Keratinocytes	29180	29.66	272.9	545.80	Keratinocytes	
B-actin control		27.64	956.41			
genomic		27.35	1143.39			
1.00E+05		20.14	100000			
1.00E+05		20.26	100000			
1.00E+04		23.6	10000			
1.00E+04		24.02	10000			
1.00E+03		27.49	1000			
1.00E+03		27.5	1000			
1.00E+02		31.66	100			
1.00E+02		31.01	100			
1.00E+01		40	0			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg1002620T1b

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.24
colon tumor	-2.37
colon tumor	-1.55
colon tumor	-2.97
lung tumor	-9.28
lung tumor	-2.02
lung tumor	-1.54
lung tumor	2.52
breast tumor	1.84
breast tumor	-1.43
breast tumor	2.40
breast tumor	-1.88
brain stage 5 ALZ	-2.15
brain stage 5 ALZ	-1.47
brain stage 5 ALZ	-1.86
brain stage 5 ALZ	-1.54
lung 24	-61.80
lung 28	-12.12

lung 23	-38.94
asthmatic lung	2.43
asthmatic lung	1.84
asthmatic lung	12.18
asthmatic lung	2.66
endo VEGF	-2.36
endo bFGF	2.77
heart T-1	1.32
heart T-14	2.86
heart T-3399	4.04
BM stim	-3.57
osteo dif	4.97
Cartilage (pool)	-1.15
PBL HIV IIIB	-1.18
MRC5 HSV strain F	-2.21

Gene Name sbg102200MCTa

- 5 Moderate to low overall expression. Highest normal expression in the subcutaneous adipose tissue, whole brain, fetal brain, cerebellum, and fetal liver. Highest disease expression in 2 of 4 lung tumor samples, one of the normal lung samples, one of the normal breast samples, and the CT lung sample. Downregulation in 1 of 4 breast cancer samples implicates this gene in cancer of the breast. Downregulation in 3 of 3 COPD lung samples suggests involvement in chronic obstructive pulmonary disease. Moderate expression in the OA and RA synovium as well as the PBLs, adenoid,
- 10 tonsil, T cells, B cells, and the chondrocytes indicates involvement in osteoarthritis and rheumatoid arthritis.

Sample sbg102200MCTa	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	36.01, 34.76	3.83	8.04	5.94	3.06	16.34	96.98
Subcutaneous Adipose Zenbio	34.85, 33.96	7.63	12.94	10.29	0.96	52.36	538.48
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	26.05, 26.18	1434.25	1331.2	1382.73	7.24	6.91	9549.21
Fetal Brain Clontech	40, 34.46	0	9.63	4.82	0.48	103.95	500.52
Cerebellum Clontech	31.7, 32.73	49.65	26.9	38.28	2.17	23.04	881.91
Cervix	40, 40	0	0	0.00	2.42	20.66	0.00
Colon	38.55, 38.57	0.84	0.83	0.84	2.71	18.45	15.41
Endometrium	40, 40	0	0	0.00	0.73	68.21	0.00
Esophagus	35.23, 40	6.09	0	3.05	1.37	36.50	111.13
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	39.8, 40	0.4	0	0.20	0.32	155.28	31.06
Ileum	34.16, 40	11.53	0	5.77	2.58	19.38	111.72
Jejunum	32.82, 33.18	25.46	20.6	23.03	6.60	7.58	174.47
Kidney	34.23, 34.1	11.02	11.9	11.46	2.12	23.58	270.28
Liver	35.35, 37.28	5.65	1.79	3.72	1.50	33.33	124.00
Fetal Liver Clontech	29.45, 28.98	189.89	250.96	220.43	10.40	4.81	1059.74

Lung	34.99, 33.43	7.04	17.81	12.43	2.57	19.46	241.73
Mammary Gland Clontech	31.76, 31.05	48.02	73.18	60.60	13.00	3.85	233.08
Myometrium	34.46, 35.22	9.64	6.12	7.88	2.34	21.37	168.38
Omentum	37.94, 34.13	1.21	11.71	6.46	3.94	12.69	81.98
Ovary	34.03, 33.43	12.44	17.77	15.11	4.34	11.52	174.02
Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	32.56, 31.81	29.88	46.65	38.27	5.48	9.12	349.13
Placenta Clontech	40, 40	0	0	0.00	5.26	9.51	0.00
Prostate	40, 36.21	0	3.39	1.70	3.00	16.67	28.25
Rectum	40, 39.37	0	0.52	0.26	1.23	40.65	10.57
Salivary Gland Clontech	30.6, 31.77	95.89	47.76	71.83	7.31	6.84	491.28
Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	34.47, 35.32	9.58	5.75	7.67	1.21	41.32	316.74
Small Intestine Clontech	40, 40	0	0	0.00	0.98	51.07	0.00
Spleen	34.1, 36.49	11.93	2.87	7.40	4.92	10.16	75.20
Stomach	35.17, 36.07	6.3	3.68	4.99	2.73	18.32	91.39
Testis Clontech	37.98, 40	1.19	0	0.60	0.57	87.87	52.28
Thymus Clontech	31.28, 30.4	63.69	108.05	85.87	9.89	5.06	434.13
Thyroid	33.08, 32.96	21.88	23.47	22.68	2.77	18.05	409.30
Trachea Clontech	32.54, 31.34	30.14	61.71	45.93	9.71	5.15	236.48
Urinary Bladder	33.91, 40	13.32	0	6.66	5.47	9.14	60.88
Uterus	33.71, 32.43	15.04	32.13	23.59	5.34	9.36	220.83
genomic	26.3	1237.42					
b-actin	27.49	610.72					
1.00E+05	19.18	100000					
1.00E+05	19.45	100000					
1.00E+04	22.6	10000					
1.00E+04	22.53	10000					
1.00E+03	26.17	1000					
1.00E+03	26.19	1000					
1.00E+02	30.61	100					
1.00E+02	30.53	100					
1.00E+01	40	0					
1.00E+01	34.91	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg102200MCTa	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detecte	Sample	Fold Change in Disease Populatio
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)			d/50 ng total RNA		n
colon normal GW98-167	21941	28.58	519.72	1039.44	colon normal	
colon tumor GW98-166	21940	30.18	202.86	405.72	colon tumor	-2.56
colon normal GW98-178	22080	31.39	100.15	200.30	colon normal	
colon tumor GW98-177	22060	29.62	282.42	564.84	colon tumor	2.82
colon normal GW98-561	23514	30.36	183.13	366.26	colon normal	
colon tumor GW98-560	23513	30.45	173.87	347.74	colon tumor	-1.05
colon normal GW98-894	24691	30.23	196.98	393.96	colon normal	
colon tumor GW98-893	24690	30.35	183.76	367.52	colon tumor	-1.07
lung normal GW98-3	20742	26.68	1575.72	3151.44	lung normal	
lung tumor GW98-2	20741	28.8	456.47	912.94	lung tumor	-3.45
lung normal GW97-179	20677	27.94	754.47	1508.94	lung normal	
lung tumor GW97-178	20676	26.27	2002.28	4004.56	lung tumor	2.65
lung normal GW98-165	21922	26.87	1411.09	2822.18	lung normal	
lung tumor GW98-164	21921	29.38	325.51	651.02	lung tumor	-4.34
lung normal GW98-282	22584	30	225.32	450.64	lung normal	
lung tumor GW98-281	22583	28.64	502.02	1004.04	lung tumor	2.23
breast normal GW00-392	28750	28.32	602.59	602.59	breast normal	
breast tumor GW00-391	28746	28.05	709.37	1418.74	breast tumor	2.35
breast normal GW00-413	28798	29.56	292.43	292.43	breast normal	
breast tumor GW00-412	28797	30.05	218.89	437.78	breast tumor	1.50
breast normal GW00-235:238	27592-95	30.96	128.91	128.91	breast normal	
breast tumor GW00-231:234	27588-91	30.57	161.3	161.30	breast tumor	1.25
breast normal GW98-621	23656	27.04	1275.81	2551.62	breast normal	
breast tumor GW98-620	23655	31.35	102.26	204.52	breast tumor	-12.48
brain normal BB99-542	25507	28.44	564.32	1128.64	brain normal	
brain normal BB99-406	25509	29.01	402.37	804.74	brain normal	
brain normal BB99-904	25546	29.67	274.03	548.06	brain normal	
brain stage 5 ALZ BB99-874	25502	29.6	284.82	569.64	brain stage 5 ALZ	-1.45
brain stage 5 ALZ BB99-887	25503	27.92	765.16	1530.32	brain stage 5 ALZ	1.85
brain stage 5 ALZ BB99-862	25504	28.74	472.27	944.54	brain stage 5 ALZ	1.14
brain stage 5 ALZ BB99-927	25542	29.3	340.25	680.50	brain stage 5 ALZ	-1.22
CT lung KC	normal	26.69	1569.87	3139.74	CT lung	
lung 26 KC	normal	31.07	120.9	120.90	lung 26	
lung 27 KC	normal	31.17	113.69	113.69	lung 27	
lung 24 KC	COPD	31.8	78.78	78.78	lung 24	-10.98
lung 28 KC	COPD	32.79	44.02	44.02	lung 28	-19.65
lung 23 KC	COPD	31.35	102.33	102.33	lung 23	-8.45
lung 25 KC	normal	31.66	85.57	85.57	lung 25	
asthmatic lung ODO3112	29321	28.76	467.45	467.45	asthmatic lung	-1.85
asthmatic lung ODO3433	29323	27.73	851.21	1702.42	asthmatic lung	1.97
asthmatic lung ODO3397	29322	27.81	812.68	1625.36	asthmatic lung	1.88

asthmatic lung ODO4928	29325	29.42	317.12	634.24	asthmatic lung	-1.36
endo cells KC	control	33.06	37.57	37.57	endo cells	
endo VEGF KC		33.9	22.97	22.97	endo VEGF	-1.64
endo bFGF KC		33.13	36.03	36.03	endo bFGF	-1.04
heart Clontech	normal	31.1	118.18	236.36	heart	
heart (T-1) ischemic	29417	31.16	114.67	229.34	heart T-1	-1.03
heart (T-14) non-obstructive DCM	29422	30.52	166.47	332.94	heart T-14	1.41
heart (T-3399) DCM	29426	30.14	208.3	416.60	heart T-3399	1.76
adenoid GW99-269	26162	29.07	388.9	777.80	adenoid	
tonsil GW98-280	22582	28.29	614.82	1229.64	tonsil	
T cells PC00314	28453	29.78	256.1	512.20	T cells	
PBMNC		33.73	25.44	25.44	PBMNC	
monocyte		33.52	28.71	57.42	monocyte	
B cells PC00665	28455	28.66	495.36	990.72	B cells	
dendritic cells 28441		30.81	140.17	280.34	dendritic cells	
neutrophils	28440	30.17	204.92	204.92	neutrophils	
eosinophils	28446	34.19	19.39	38.78	eosinophils	
BM unstim		35.9	7.11	7.11	BM unstim	
BM stim		35.77	7.7	7.70	BM stim	1.08
osteo dif		34.98	12.18	12.18	osteo dif	2.55
osteo undif		36.59	4.77	4.77	osteo undif	
chondrocytes		32.91	41.03	102.58	chondrocytes	
OA Synovium IP12/01	29462	29.16	370.33	370.33	OA Synovium	
OA Synovium NP10/01	29461	30.69	151.13	302.26	OA Synovium	
OA Synovium NP57/00	28464	29.51	301.55	603.10	OA Synovium	
RA Synovium NP03/01	28466	30.36	183.35	366.70	RA Synovium	
RA Synovium NP71/00	28467	29.27	346.61	693.22	RA Synovium	
RA Synovium NP45/00	28475	29.13	376.88	753.76	RA Synovium	
OA bone (biobank)	29217	30.47	171.6	171.60	OA bone (biobank)	
OA bone Sample 1	J. Emory	30.05	219.19	438.38	OA bone	
OA bone Sample 2	J. Emory	31.13	116.62	233.24	OA bone	
Cartilage (pool)	Normal	30.65	154.56	309.12	Cartilage (pool)	
Cartilage (pool)	OA	32.01	69.39	138.78	Cartilage (pool)	-2.23
PBL uninfected	28441	27.91	769.91	1539.82	PBL uninfected	
PBL HIV IIIB	28442	28.14	672.12	1344.24	PBL HIV IIIB	-1.15
MRC5 uninfected (100%)	29158	31.66	85.38	170.76	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	30.08	214.88	429.76	MRC5 HSV strain F	2.52
W12 cells	29179	33.33	32.15	64.30	W12 cells	
Keratinocytes	29180	30.64	155.16	310.32	Keratinocytes	
B-actin control		27.55	946.64			
genomic		26.82	1451.22			
1.00E+05		19.71	100000			
1.00E+05		19.95	100000			
1.00E+04		23.43	10000			
1.00E+04		23.38	10000			

1.00E+03		26.88	1000			
1.00E+03		26.8	1000			
1.00E+02		31.99	100			
1.00E+02		32.15	100			
1.00E+01		34.99	10			
1.00E+01		40	0			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg102200MCTa

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-2.56
colon tumor	2.82
colon tumor	-1.05
colon tumor	-1.07
lung tumor	-3.45
lung tumor	2.65
lung tumor	-4.34
lung tumor	2.23
breast tumor	2.35
breast tumor	1.50
breast tumor	1.25
breast tumor	-12.48
brain stage 5 ALZ	-1.45
brain stage 5 ALZ	1.85
brain stage 5 ALZ	1.14
brain stage 5 ALZ	-1.22
lung 24	-10.98
lung 28	-19.65
lung 23	-8.45
asthmatic lung	-1.85
asthmatic lung	1.97
asthmatic lung	1.88
asthmatic lung	-1.36
endo VEGF	-1.64
endo bFGF	-1.04
heart T-1	-1.03
heart T-14	1.41
heart T-3399	1.76
BM stim	1.08
osteo dif	2.55
Cartilage (pool)	-2.23
PBL HIV IIIB	-1.15
MRC5 HSV strain F	2.52

Gene Name sbg102200MCTb

- 5 High to moderate overall expression. Highest normal expression in the whole brain, liver, fetal liver, and thymus. Highest disease expression in one of the colon normal/tumor pairs, one of the lung normal/tumor pairs, one of the asthmatic lung samples, the dendritic cells, and the uninfected and HIV-infected PBL cells. Upregulation in 2 of 4 breast tumor samples is sufficient to make a disease claim in cancer of the breast. Upregulation in 1 of 4 AD brain samples indicates a potential role in Alzheimer's disease. Downregulation in 3 of 3 COPD lung samples suggests involvement in chronic obstructive pulmonary disease. Upregulation in 1 of 4 asthmatic lung samples indicates a potential role for this gene in lung cancer. High expression in all of the immune cells. Also high to moderate expression in the OA and RA synovium samples, the OA bone samples, and in the chondrocytes suggests an involvement in osteoarthritis and rheumatoid arthritis.
- 10

Sample sbg102200MCTb	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	35.66, 34.05	3.76	10.2	6.98	3.06	16.34	114.05
Subcutaneous Adipose Zenbio	40, 36	0.17	3.07	1.62	0.96	52.36	84.82
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	26.32, 26.41	1192.66	1124.69	1158.68	7.24	6.91	8001.90
Fetal Brain Clontech	40, 35.84	0	3.38	1.69	0.48	103.95	175.68
Cerebellum Clontech	34.51, 34.28	7.68	8.8	8.24	2.17	23.04	189.86
Cervix	40, 34.34	3.17	8.5	5.84	2.42	20.66	120.56
Colon	33.67, 35.6	12.86	3.91	8.39	2.71	18.45	154.70
Endometrium	35.32, 34.43	4.66	8.05	6.36	0.73	68.21	433.49
Esophagus	34.27, 35.14	8.86	5.19	7.03	1.37	36.50	256.39
Heart Clontech	40, 35.05	0	5.5	2.75	1.32	37.88	104.17
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	35.29, 33.68	4.74	12.8	8.77	2.58	19.38	169.96
Jejunum	31.23, 30.98	57.65	67.22	62.44	6.60	7.58	472.99
Kidney	34.67, 34.21	6.95	9.2	8.08	2.12	23.58	190.45
Liver	30.76, 30.65	77.12	82.56	79.84	1.50	33.33	2661.33
Fetal Liver Clontech	26.8, 27.1	885.14	734.31	809.73	10.40	4.81	3892.91
Lung	40, 40	0	0.17	0.09	2.57	19.46	1.65
Mammary Gland Clontech	31.28, 31.37	56.1	52.95	54.53	13.00	3.85	209.71
Myometrium	34.16, 36.28	9.48	2.57	6.03	2.34	21.37	128.74
Omentum	34.18, 33.42	9.38	15	12.19	3.94	12.69	154.70
Ovary	34.21, 34.18	9.24	9.39	9.32	4.34	11.52	107.32
Pancreas	40, 40	0	0.14	0.07	0.81	61.80	4.33
Head of Pancreas	40, 35.02	0	5.59	2.80	1.57	31.85	89.01
Parotid Gland	31.23, 31.9	57.68	38.33	48.01	5.48	9.12	438.00
Placenta Clontech	31.77, 33.13	41.33	17.94	29.64	5.26	9.51	281.70
Prostate	39.72, 35.03	0.31	5.56	2.94	3.00	16.67	48.92
Rectum	35.36, 34.34	4.53	8.5	6.52	1.23	40.65	264.84
Salivary Gland Clontech	30.52, 30.54	89.5	88.43	88.97	7.31	6.84	608.52

Skeletal Muscle Clontech	40, 40	0	0	0.00	1.26	39.68	0.00
Skin	40, 40	0	0	0.00	1.21	41.32	0.00
Small Intestine Clontech	40, 39.27	0	0.41	0.21	0.98	51.07	10.47
Spleen	34.21, 33.54	9.2	13.91	11.56	4.92	10.16	117.43
Stomach	35.05, 33.62	5.51	13.22	9.37	2.73	18.32	171.52
Testis Clontech	40, 40	0	0	0.00	0.57	87.87	0.00
Thymus Clontech	28.56, 28.44	299.45	322.02	310.74	9.89	5.06	1570.96
Thyroid	31.65, 32.3	44.76	29.81	37.29	2.77	18.05	673.01
Trachea Clontech	32.3, 31.9	29.9	38.28	34.09	9.71	5.15	175.54
Urinary Bladder	34.34, 35.02	8.49	5.59	7.04	5.47	9.14	64.35
Uterus	33.07, 34.56	18.62	7.45	13.04	5.34	9.36	122.05
genomic	25.84	1597.08					
b-actin	27.32	643.56					
1.00E+05	19.22	100000					
1.00E+05	19.33	100000					
1.00E+04	22.48	10000					
1.00E+04	22.95	10000					
1.00E+03	26.19	1000					
1.00E+03	26.37	1000					
1.00E+02	31.23	100					
1.00E+02	30.48	100					
1.00E+01	32.76	10					
1.00E+01	35.02	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample sbg102200MCTb	Reg number (GSK identifie r)	Ct	Mean GOI copies	copies of mRNA detected /50 ng total RNA	Sample	Fold Change in Disease Populati on
colon normal GW98-167	21941	26.48	1723.59	3447.18	colon normal	
colon tumor GW98-166	21940	26.06	2195.04	4390.08	colon tumor	1.27
colon normal GW98-178	22080	29.03	389.88	779.76	colon normal	
colon tumor GW98-177	22060	27.39	1015.65	2031.30	colon tumor	2.61
colon normal GW98-561	23514	26.74	1478.76	2957.52	colon normal	
colon tumor GW98-560	23513	26.37	1831.8	3663.60	colon tumor	1.24
colon normal GW98-894	24691	25.58	2918.02	5836.04	colon normal	
colon tumor GW98-893	24690	25	4089.75	8179.50	colon tumor	1.40
lung normal GW98-3	20742	24.59	5183.31	10366.62	lung normal	
lung tumor GW98-2	20741	24.94	4232.23	8464.46	lung tumor	-1.22
lung normal GW97-179	20677	25.73	2672.73	5345.46	lung normal	
lung tumor GW97-178	20676	25.36	3307.37	6614.74	lung tumor	1.24
lung normal GW98-165	21922	26.13	2109.28	4218.56	lung normal	

lung tumor GW98-164	21921	25.54	2973.82	5947.64	lung tumor	1.41
lung normal GW98-282	22584	27.08	1212.64	2425.28	lung normal	
lung tumor GW98-281	22583	27.45	979.82	1959.64	lung tumor	-1.24
breast normal GW00-392	28750	26.68	1536.57	1536.57	breast normal	
breast tumor GW00-391	28746	26.58	1626.58	3253.16	breast tumor	2.12
breast normal GW00-413	28798	31.71	81.9	81.90	breast normal	
breast tumor GW00-412	28797	26.57	1632	3264.00	breast tumor	39.85
breast normal GW00-235:238	27592-95	32.52	51.1	51.10	breast normal	
breast tumor GW00-231:234	27588-91	29.67	268.7	268.70	breast tumor	5.26
breast normal GW98-621	23656	26.48	1727.44	3454.88	breast normal	
breast tumor GW98-620	23655	25.65	2793.6	5587.20	breast tumor	1.62
brain normal BB99-542	25507	28.62	494	988.00	brain normal	
brain normal BB99-406	25509	29.45	304.68	609.36	brain normal	
brain normal BB99-904	25546	30.08	211.25	422.50	brain normal	
brain stage 5 ALZ BB99-874	25502	28.75	458.64	917.28	brain stage 5 ALZ	1.36
brain stage 5 ALZ BB99-887	25503	26.86	1383.71	2767.42	brain stage 5 ALZ	4.11
brain stage 5 ALZ BB99-862	25504	28.02	702.59	1405.18	brain stage 5 ALZ	2.09
brain stage 5 ALZ BB99-927	25542	29.57	284.31	568.62	brain stage 5 ALZ	-1.18
CT lung KC	normal	26.58	1624.29	3248.58	CT lung	
lung 26 KC	normal	34.19	19.27	19.27	lung 26	
lung 27 KC	normal	32.45	53.23	53.23	lung 27	
lung 24 KC	COPD	33	38.6	38.60	lung 24	-21.75
lung 28 KC	COPD	32.24	59.95	59.95	lung 28	-14.01
lung 23 KC	COPD	32.87	41.63	41.63	lung 23	-20.17
lung 25 KC	normal	33.04	37.52	37.52	lung 25	
asthmatic lung ODO3112	29321	30.13	205.46	205.46	asthmatic lung	-4.09
asthmatic lung ODO3433	29323	27.82	788.82	1577.64	asthmatic lung	1.88
asthmatic lung ODO3397	29322	25.17	3695.43	7390.86	asthmatic lung	8.80
asthmatic lung ODO4928	29325	27.6	894.3	1788.60	asthmatic lung	2.13
endo cells KC	control	28.2	633.43	633.43	endo cells	
endo VEGF KC		28.86	429.51	429.51	endo VEGF	-1.47
endo bFGF KC		28.97	403.08	403.08	endo bFGF	-1.57
heart Clontech	normal	28.83	437.62	875.24	heart	
heart (T-1) ischemic	29417	28.42	557.54	1115.08	heart T-1	1.27
heart (T-14) non-obstructive DCM	29422	27.72	835.11	1670.22	heart T-14	1.91
heart (T-3399) DCM	29426	28.63	493.01	986.02	heart T-3399	1.13
adenoid GW99-269	26162	27	1269.75	2539.50	adenoid	
tonsil GW98-280	22582	26.33	1876.29	3752.58	tonsil	
T cells PC00314	28453	29.15	363.35	726.70	T cells	
PBMNC		33.05	37.41	37.41	PBMNC	
monocyte		31.49	92.84	185.68	monocyte	
B cells PC00665	28455	26.5	1700.87	3401.74	B cells	
dendritic cells 28441		24.2	6511.17	13022.34	dendritic cells	

neutrophils	28440	27.01	1262.74	1262.74	neutrophils	
eosinophils	28446	29.23	347.08	694.16	eosinophils	
BM unstim		30.85	135.01	135.01	BM unstim	
BM stim		28.68	478.5	478.50	BM stim	3.54
osteo dif		31.03	121.2	121.20	osteo dif	3.93
osteo undif		33.38	30.85	30.85	osteo undif	
chondrocytes		26.63	1579.73	3949.33	chondrocytes	
OA Synovium IP12/01	29462	29.11	371.98	371.98	OA Synovium	
OA Synovium NP10/01	29461	29.45	304.55	609.10	OA Synovium	
OA Synovium NP57/00	28464	27.83	784.87	1569.74	OA Synovium	
RA Synovium NP03/01	28466	27.31	1063.77	2127.54	RA Synovium	
RA Synovium NP71/00	28467	27.08	1217.21	2434.42	RA Synovium	
RA Synovium NP45/00	28475	26.6	1606.41	3212.82	RA Synovium	
OA bone (biobank)	29217	28.65	485.63	485.63	OA bone (biobank)	
OA bone Sample 1	J. Emory	28.78	451.74	903.48	OA bone	
OA bone Sample 2	J. Emory	28.27	607.15	1214.30	OA bone	
Cartilage (pool)	Normal	29.42	310.76	621.52	Cartilage (pool)	
Cartilage (pool)	OA	30.09	209.7	419.40	Cartilage (pool)	-1.48
PBL uninfected	28441	23.85	7997.03	15994.06	PBL uninfected	
PBL HIV IIIB	28442	24.85	4447.34	8894.68	PBL HIV IIIB	-1.80
MRC5 uninfected (100%)	29158	27.02	1258.46	2516.92	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	29.6	278.84	557.68	MRC5 HSV strain F	-4.51
W12 cells	29179	27.21	1122.77	2245.54	W12 cells	
Keratinocytes	29180	25.64	2815.12	5630.24	Keratinocytes	
B-actin control		27.78	807.72			
genomic		27.04	1246.22			
1.00E+05		19.69	100000			
1.00E+05		20.01	100000			
1.00E+04		23.15	10000			
1.00E+04		23.2	10000			
1.00E+03		27.02	1000			
1.00E+03		26.76	1000			
1.00E+02		31.45	100			
1.00E+02		32.39	100			
1.00E+01		35.72	10			
1.00E+01		34.74	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			

Gene Name sbg102200MCTb

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.27
colon tumor	2.61
colon tumor	1.24

colon tumor	1.40
lung tumor	-1.22
lung tumor	1.24
lung tumor	1.41
lung tumor	-1.24
breast tumor	2.12
breast tumor	39.85
breast tumor	5.26
breast tumor	1.62
brain stage 5 ALZ	1.36
brain stage 5 ALZ	4.11
brain stage 5 ALZ	2.09
brain stage 5 ALZ	-1.18
lung 24	-21.75
lung 28	-14.01
lung 23	-20.17
asthmatic lung	-4.09
asthmatic lung	1.88
asthmatic lung	8.80
asthmatic lung	2.13
endo VEGF	-1.47
endo bFGF	-1.57
heart T-1	1.27
heart T-14	1.91
heart T-3399	1.13
BM stim	3.54
osteo dif	3.93
Cartilage (pool)	-1.48
PBL HIV IIIB	-1.80
MRC5 HSV strain F	-4.51

Gene Name sbg1020380LYG

Failed

5

Gene Name sbg1007026SGLT

Good to moderate overall expression. The highest normal expression is seen in the whole brain, cerebellum, hypothalamus, jejunum, fetal liver, rectum, and uterus. This gene shows system specific expression in samples representing the central nervous system, the female reproductive organs, and the GI tract. The expression seen in the disease samples confirms that seen in the normal samples with the highest levels of expression seen in the normal and Alzheimer's brain samples. Upregulation in 1 of 4 colon tumor samples and 2 of 4 breast tumor samples as well as downregulation in 1 of 4 lung tumors poses a potential role for this gene in cancers of the colon and breast. Downregulation in 2 of 4 Alzheimer's brain samples implies involvement in Alzheimer's disease. Downregulation in 3 of 3 COPD samples and upregulation in 2 of 4 asthmatic lung samples suggests a potential role for this gene in chronic obstructive pulmonary disorder. Upregulation in the VEGF-treated endothelial cell line implicates a possible role for this gene in angiogenesis. Downregulated in the stimulated bone marrow sample. High expression in the RA and OA synovium samples, the OA bone samples, and the chondrocytes with corroborating high expression in the T cells, B cells, neutrophils, and eosinophils implicates this gene in osteoarthritis and rheumatoid arthritis.

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15

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Sample	Ct (sample 1 and 2)	Mean GOI	Mean GOI	Average GOI	18S rRNA	50 ng/18	copies of mRNA
sbg1007026SGLT							

		copies (sample 1)	copies (sample 2)	Copies	(ng)	S rRNA (ng)	detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 40	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	40, 40	0	0.1	0.05	0.96	52.36	2.62
Adrenal Gland Clontech	40, 38.76	0	0.31	0.16	0.61	81.97	12.70
Whole Brain Clontech	23.01, 22.63	3438.45	4301.69	3870.07	7.24	6.91	26727.00
Fetal Brain Clontech	35.91, 39.16	1.66	0.24	0.95	0.48	103.95	98.75
Cerebellum Clontech	34.55, 32.7	3.71	11.08	7.40	2.17	23.04	170.39
Cervix	34.21, 34.61	4.54	3.58	4.06	2.42	20.66	83.88
Colon	33.44, 33.7	7.16	6.14	6.65	2.71	18.45	122.69
Endometrium	34.88, 40	3.05	0.1	1.58	0.73	68.21	107.44
Esophagus	40, 40	0	0.1	0.05	1.37	36.50	1.82
Heart Clontech	39.63, 39.53	0.18	0.19	0.19	1.32	37.88	7.01
Hypothalamus	40, 35.34	0	2.33	1.17	0.32	155.28	180.90
Ileum	40, 40	0	0	0.00	2.58	19.38	0.00
Jejunum	30.1, 30.34	51.59	44.92	48.26	6.60	7.58	365.57
Kidney	33.49, 40	6.96	0	3.48	2.12	23.58	82.08
Liver	40, 33.7	0	6.15	3.08	1.50	33.33	102.50
Fetal Liver Clontech	29.58, 29.41	70.26	77.58	73.92	10.40	4.81	355.38
Lung	35.61, 37.83	1.98	0.53	1.26	2.57	19.46	24.42
Mammary Gland Clontech	33.05, 34.04	9.02	5.03	7.03	13.00	3.85	27.02
Myometrium	33.63, 34.13	6.38	4.77	5.58	2.34	21.37	119.12
Omentum	40, 40	0	0	0.00	3.94	12.69	0.00
Ovary	35.38, 37.6	2.27	0.61	1.44	4.34	11.52	16.59
Pancreas	40, 37.1	0	0.82	0.41	0.81	61.80	25.34
Head of Pancreas	35.45, 36.72	2.18	1.03	1.61	1.57	31.85	51.11
Parotid Gland	36.88, 40	0.94	0	0.47	5.48	9.12	4.29
Placenta Clontech	33.84, 38.46	5.66	0.37	3.02	5.26	9.51	28.66
Prostate	38.76, 37.12	0.31	0.81	0.56	3.00	16.67	9.33
Rectum	36.18, 33.82	1.42	5.7	3.56	1.23	40.65	144.72
Salivary Gland Clontech	38.36, 39.93	0.39	0.12	0.26	7.31	6.84	1.74
Skeletal Muscle Clontech	35.69, 36.23	1.9	1.38	1.64	1.26	39.68	65.08
Skin	39.51, 40	0.2	0.09	0.15	1.21	41.32	5.99
Small Intestine Clontech	40, 36.04	0.1	1.53	0.82	0.98	51.07	41.62
Spleen	33.51, 38.51	6.87	0.36	3.62	4.92	10.16	36.74
Stomach	34.14, 34.19	4.73	4.59	4.66	2.73	18.32	85.35
Testis Clontech	35.81, 40	1.76	0.11	0.94	0.57	87.87	82.16
Thymus Clontech	33.26, 32.49	7.96	12.55	10.26	9.89	5.06	51.85
Thyroid	40, 39.9	0.08	0.16	0.12	2.77	18.05	2.17
Trachea Clontech	34.25, 33.8	4.42	5.77	5.10	9.71	5.15	26.24
Urinary Bladder	39.95, 36.54	0.1	1.14	0.62	5.47	9.14	5.67
Uterus	33, 31.23	9.3	26.52	17.91	5.34	9.36	167.70
genomic	24.72	1251.19					

b-actin	25.89	625.04					
1.00E+05	17.54	100000					
1.00E+05	17.65	100000					
1.00E+04	21.03	10000					
1.00E+04	20.92	10000					
1.00E+03	24.87	1000					
1.00E+03	24.96	1000					
1.00E+02	29.1	100					
1.00E+02	29.04	100					
1.00E+01	32.05	10					
1.00E+01	33.51	10					
1.00E-00	36.41	1					
1.00E-00	37.41	1					
NTC	40	0					
NTC	40	-1					

Sample sbg1007026SGLT	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detected/ 50 ng total RNA	Sample	Fold Change in Disease Populati on
colon normal GW98-167	21941	29.22	127.1	254.20	colon normal	
colon tumor GW98-166	21940	31.07	44.11	88.22	colon tumor	-2.88
colon normal GW98-178	22080	38.41	0.65	1.30	colon normal	
colon tumor GW98-177	22060	31.17	41.5	83.00	colon tumor	63.85
colon normal GW98-561	23514	31.21	40.69	81.38	colon normal	
colon tumor GW98-560	23513	33.06	14.04	28.08	colon tumor	-2.90
colon normal GW98-894	24691	29.63	100.41	200.82	colon normal	
colon tumor GW98-893	24690	32.22	22.7	45.40	colon tumor	-4.42
lung normal GW98-3	20742	29.8	91.46	182.92	lung normal	
lung tumor GW98-2	20741	34.26	7.02	14.04	lung tumor	-13.03
lung normal GW97-179	20677	29.59	103.13	206.26	lung normal	
lung tumor GW97-178	20676	29.84	89.09	178.18	lung tumor	-1.16
lung normal GW98-165	21922	29.6	102.46	204.92	lung normal	
lung tumor GW98-164	21921	30.8	51.53	103.06	lung tumor	-1.99
lung normal GW98-282	22584	32.53	18.97	37.94	lung normal	
lung tumor GW98-281	22583	32.29	21.8	43.60	lung tumor	1.15
breast normal GW00-392	28750	28.77	164.85	164.85	breast normal	
breast tumor GW00-391	28746	30.64	56.21	112.42	breast tumor	-1.47
breast normal GW00-413	28798	34.49	6.17	6.17	breast normal	
breast tumor GW00-412	28797	30.37	65.97	131.94	breast tumor	21.38
breast normal GW00-235:238	27592-95	32.87	15.66	15.66	breast normal	
breast tumor GW00-231:234	27588-91	29.8	91.07	91.07	breast tumor	5.82
breast normal GW98-621	23656	28.95	149.19	298.38	breast normal	
breast tumor GW98-620	23655	29.62	101.25	202.50	breast tumor	-1.47
brain normal BB99-542	25507	24.5	1917.28	3834.56	brain normal	

brain normal BB99-406	25509	21.35	11736.92	23473.84	brain normal	
brain normal BB99-904	25546	25.25	1248.68	2497.36	brain normal	
brain stage 5 ALZ BB99-874	25502	27.29	386.81	773.62	brain stage 5 ALZ	-12.84
brain stage 5 ALZ BB99-887	25503	23.61	3196.37	6392.74	brain stage 5 ALZ	-1.55
brain stage 5 ALZ BB99-862	25504	25.56	1045.09	2090.18	brain stage 5 ALZ	-4.75
brain stage 5 ALZ BB99-927	25542	24.45	1976.24	3952.48	brain stage 5 ALZ	-2.51
CT lung	normal	31.07	44.03	88.06	CT lung Nml	
lung 26	normal	24.93	1496.87		lung 26 Nml	
lung 27	normal	34.06	7.92	7.92	lung 27 Nml	
lung 24	COPD	34.58	5.87	5.87	lung 24 COPD	-5.45
lung 28	COPD	40	0	0.00	lung 28 COPD	-31.99
lung 23	COPD	40	0	0.00	lung 23 COPD	-31.99
lung 25	normal	40	0	0.00	lung 25 Nml	
asthmatic lung ODO3112	29321	33.19	13.04	13.04	asthmatic lung	-2.45
asthmatic lung ODO3433	29323	30.61	57.38	114.76	asthmatic lung	3.59
asthmatic lung ODO3397	29322	29.2	129.16	258.32	asthmatic lung	8.07
asthmatic lung ODO4928	29325	30.32	67.67	135.34	asthmatic lung	4.23
endo cells	control	35.09	4.37	4.37	endo cells	
endo VEGF		32.22	22.7	22.70	endo VEGF	5.19
endo bFGF		33.23	12.7	12.70	endo bFGF	2.91
heart Clontech	normal	33.53	10.71	21.42	heart	
heart (T-1) ischemic	29417	33.43	11.37	22.74	heart (T-1) ischemic	1.06
heart (T-14) non-obstructive DCM	29422	34.45	6.32	12.64	heart (T-14) non-obstructive DCM	-1.69
heart (T-3399) DCM	29426	31.98	26.02	52.04	heart (T-3399) DCM	2.43
adenoid GW99-269	26162	29.56	104.93	209.86	adenoid	
tonsil GW98-280	22582	29	144.55	289.10	tonsil	
T cells PC00314	28453	32.03	25.34	50.68	T cells	
PBMNC		37.71	0.97	0.97	PBMNC	
monocyte		37.49	1.1	2.20	monocyte	
B cells PC00665	28455	27.18	410.49	820.98	B cells	
dendritic cells	28441	33.7	9.73	19.46	dendritic cells	
neutrophils	28440	32.48	19.6	19.60	neutrophils	
eosinophils	28446	32.44	20.08	40.16	eosinophils	
BM unstim		33.8	9.17	9.17	BM unstim	
BM stim	treated	38.89	0.49	0.49	BM stim	-18.71
osteo dif	treated	37.26	1.26	1.26	osteo dif	1.26
osteo undif		40	0	0.00	osteo undif	
chondrocytes		32.07	24.82	62.05	chondrocytes	
OA Synovium IP12/01	29462	30.31	68.26	68.26	OA Synovium	
OA Synovium NP10/01	29461	30.74	53.26	106.52	OA Synovium	
OA Synovium NP57/00	28464	31.3	38.48	76.96	OA Synovium	
RA Synovium NP03/01	28466	31.08	43.89	87.78	RA Synovium	
RA Synovium NP71/00	28467	31.35	37.58	75.16	RA Synovium	

RA Synovium NP45/00	28475	30.74	53.21	106.42	RA Synovium	
OA bone (biobank)	29217	30.47	61.99	61.99	OA bone (biobank)	
OA bone Sample 1	J. Emory	29.92	85.09	170.18	OA bone	
OA bone Sample 2	J. Emory	30.91	48.27	96.54	OA bone	
Cartilage (pool)	Normal	31.34	37.68	75.36	Nml Cartilage (pool)	
Cartilage (pool)	OA	31.72	30.35	60.70	OA Cartilage (pool)	-1.24
PBL uninfected	28441	30.8	51.54	103.08	PBL uninfected	
PBL HIV IIIB	28442	32.03	25.38	50.76	PBL HIV IIIB	-2.03
MRC5 uninfected (100%)	29158	32.29	21.85	43.70	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	31.21	40.73	81.46	MRC5 HSV strain F	1.86
W12 cells	29179	33.12	13.52	27.04	W12 cells	
Keratinocytes	29180	32.35	21.06	42.12	Keratinocytes	
B-actin control		25.63	1002.01			
genomic		25.19	1290.48			
1.00E+05		17.86	100000			
1.00E+05		17.85	100000			
1.00E+04		21.44	10000			
1.00E+04		21.51	10000			
1.00E+03		25.33	1000			
1.00E+03		25.26	1000			
1.00E+02		29.62	100			
1.00E+02		30.55	100			
1.00E+01		32.93	10			
1.00E+01		33.46	10			
1.00E-00		38.18	1			
1.00E-00		40	0			
NTC		38.28	-1			
*lung 26 Normal has been omitted due to multiple amplification failures from that sample						

Gene Name sbg1007026SGLT

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-2.88
colon tumor	63.85
colon tumor	-2.90
colon tumor	-4.42
lung tumor	-13.03
lung tumor	-1.16
lung tumor	-1.99
lung tumor	1.15
breast tumor	-1.47
breast tumor	21.38

breast tumor	5.82
breast tumor	-1.47
brain stage 5 ALZ	-12.84
brain stage 5 ALZ	-1.55
brain stage 5 ALZ	-4.75
brain stage 5 ALZ	-2.51
lung 24	-5.45
lung 28	-31.99
lung 23	-31.99
asthmatic lung	-2.45
asthmatic lung	3.59
asthmatic lung	8.07
asthmatic lung	4.23
endo VEGF	5.19
endo bFGF	2.91
heart T-1	1.06
heart T-14	-1.69
heart T-3399	2.43
BM stim	-18.71
osteo dif	1.26
Cartilage (pool)	-1.24
PBL HIV IIIB	-2.03
MRC5 HSV strain F	1.86

Gene Name sbg1012732GLUT

High to moderate overall expression. This gene is expressed fairly ubiquitously in all normal samples analyzed with highest levels of expression seen in the whole brain, fetal brain cerebellum, kidney, fetal liver, and the placenta. This gene is also expressed fairly ubiquitously in the disease samples. Downregulation in 3 of 3 COPD samples suggests a potential role for this gene in chronic obstructive pulmonary disorder. Upregulation in 3 of 3 disease heart samples implies an involvement in cardiovascular diseases such as non-obstructive and obstructive DCM and ischemia. Downregulation in the HSV-infected MRC5 cells suggests that this gene may play a role in HSV. Upregulated in the differentiated osteoblasts. High expression in the RA and OA synovium samples, the OA bone samples, and the chondrocytes with corroborating high expression in the T cells, B cells, dendritic cells, neutrophils, and eosinophils implicates this gene in osteoarthritis and rheumatoid arthritis.

Sample sbg1012732GLUT	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	30.84, 30.49	46.76	57.63	52.20	3.06	16.34	852.86
Subcutaneous Adipose Zenbio	34.89, 35.19	4.31	3.62	3.97	0.96	52.36	207.59
Adrenal Gland Clontech	33.79, 32.74	8.27	15.31	11.79	0.61	81.97	966.39
Whole Brain Clontech	22.02, 21.91	8374.61	8944.05	8659.33	7.24	6.91	59802.00
Fetal Brain Clontech	32.03, 32.85	23.23	14.34	18.79	0.48	103.95	1952.70
Cerebellum Clontech	28.2, 28.26	221.12	213.07	217.10	2.17	23.04	5002.19
Cervix	32.91, 34.54	13.81	5.31	9.56	2.42	20.66	197.52
Colon	30.88, 32.48	45.58	17.87	31.73	2.71	18.45	585.33
Endometrium	36.13, 32.5	2.08	17.6	9.84	0.73	68.21	671.21

Esophagus	32.19, 33.5	21.15	9.77	15.46	1.37	36.50	564.23
Heart Clontech	31.93, 31.73	24.67	27.76	26.22	1.32	37.88	992.99
Hypothalamus	40, 32.77	0	15.04	7.52	0.32	155.28	1167.70
Ileum	30.94, 30.52	44.17	56.37	50.27	2.58	19.38	974.22
Jejunum	30.04, 29.34	75.03	113.25	94.14	6.60	7.58	713.18
Kidney	29.72, 29.18	90.58	124.19	107.39	2.12	23.58	2532.67
Liver	34.81, 32.2	4.52	21.05	12.79	1.50	33.33	426.17
Fetal Liver Clontech	26.6, 26.85	567.46	488.36	527.91	10.40	4.81	2538.03
Lung	31.61, 30.52	29.69	56.54	43.12	2.57	19.46	838.81
Mammary Gland Clontech	28.06, 27.59	239.58	316.2	277.89	13.00	3.85	1068.81
Myometrium	30.44, 29.88	59.31	82.52	70.92	2.34	21.37	1515.28
Omentum	31.7, 30.82	28.2	47.35	37.78	3.94	12.69	479.38
Ovary	30.92, 31.56	44.74	30.55	37.65	4.34	11.52	433.70
Pancreas	33.08, 32.66	12.54	16.03	14.29	0.81	61.80	882.88
Head of Pancreas	33.98, 34.1	7.36	6.89	7.13	1.57	31.85	226.91
Parotid Gland	29.5, 30.55	102.86	55.41	79.14	5.48	9.12	722.03
Placenta Clontech	25.63, 25.87	1002.18	869.55	935.87	5.26	9.51	8896.06
Prostate	30.23, 31.17	67.04	38.48	52.76	3.00	16.67	879.33
Rectum	31.29, 31.15	35.89	38.94	37.42	1.23	40.65	1520.93
Salivary Gland Clontech	28.82, 28.83	153.9	152.53	153.22	7.31	6.84	1047.98
Skeletal Muscle Clontech	33.23, 32.66	11.48	16.02	13.75	1.26	39.68	545.63
Skin	32.62, 32.57	16.46	16.96	16.71	1.21	41.32	690.50
Small Intestine Clontech	34.63, 32.82	5.03	14.62	9.83	0.98	51.07	501.79
Spleen	31.45, 32.71	32.66	15.56	24.11	4.92	10.16	245.02
Stomach	32.38, 32.43	18.93	18.41	18.67	2.73	18.32	341.94
Testis Clontech	32.32, 32.27	19.58	20.17	19.88	0.57	87.87	1746.49
Thymus Clontech	27.24, 26.75	388.32	518.55	453.44	9.89	5.06	2292.39
Thyroid	30.48, 29.44	57.86	106.5	82.18	2.77	18.05	1483.39
Trachea Clontech	29.96, 30.29	78.48	64.81	71.65	9.71	5.15	368.92
Urinary Bladder	30.59, 30.1	54.25	72.45	63.35	5.47	9.14	579.07
Uterus	30.62, 29.73	53.18	89.72	71.45	5.34	9.36	669.01
genomic	25.15	1330.24					
b-actin	26.01	800.58					
1.00E+05	18.01	100000					
1.00E+05	18.19	100000					
1.00E+04	21.35	10000					
1.00E+04	21.3	10000					
1.00E+03	25.59	1000					
1.00E+03	25.51	1000					
1.00E+02	29.95	100					
1.00E+02	29.37	100					
1.00E+01	34.05	10					
1.00E+01	33.22	10					
1.00E-00	37.19	1					
1.00E-00	40	0					
NTC	40	0					

NTC	40	0					
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Sample sbg1012732GLUT	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detected/ 50 ng total RNA	Sample	Fold Change in Disease Populati on
colon normal GW98-167	21941	25.38	1695.47	3390.94	colon normal	
colon tumor GW98-166	21940	25.51	1576.91	3153.82	colon tumor	-1.08
colon normal GW98-178	22080	26.8	765.5	1531.00	colon normal	
colon tumor GW98-177	22060	25.86	1297.34	2594.68	colon tumor	1.69
colon normal GW98-561	23514	26.12	1120.64	2241.28	colon normal	
colon tumor GW98-560	23513	26.12	1121.89	2243.78	colon tumor	1.00
colon normal GW98-894	24691	24.85	2283.56	4567.12	colon normal	
colon tumor GW98-893	24690	24.37	2989.5	5979.00	colon tumor	1.31
lung normal GW98-3	20742	24.37	2984.11	5968.22	lung normal	
lung tumor GW98-2	20741	25.38	1691.06	3382.12	lung tumor	-1.76
lung normal GW97-179	20677	25.07	2020.52	4041.04	lung normal	
lung tumor GW97-178	20676	24.61	2607.03	5214.06	lung tumor	1.29
lung normal GW98-165	21922	24.92	2195.85	4391.70	lung normal	
lung tumor GW98-164	21921	25.36	1712.62	3425.24	lung tumor	-1.28
lung normal GW98-282	22584	26.24	1049.97	2099.94	lung normal	
lung tumor GW98-281	22583	25.94	1241.8	2483.60	lung tumor	1.18
breast normal GW00-392	28750	25.26	1813.7	1813.70	breast normal	
breast tumor GW00-391	28746	24.87	2259.54	4519.08	breast tumor	2.49
breast normal GW00-413	28798	25.4	1672.46	1672.46	breast normal	
breast tumor GW00-412	28797	25.21	1864.18	3728.36	breast tumor	2.23
breast normal GW00-235:238	27592-95	25.68	1435.2	1435.20	breast normal	
breast tumor GW00-231:234	27588-91	24.08	3510.78	3510.78	breast tumor	2.45
breast normal GW98-621	23656	24.16	3363.26	6726.52	breast normal	
breast tumor GW98-620	23655	24.19	3300.23	6600.46	breast tumor	-1.02
brain normal BB99-542	25507	22.64	7880.57	15761.14	brain normal	
brain normal BB99-406	25509	23.32	5357.05	10714.10	brain normal	
brain normal BB99-904	25546	23.66	4436.27	8872.54	brain normal	
brain stage 5 ALZ BB99-874	25502	24.7	2474.23	4948.46	brain stage 5 ALZ	-2.38
brain stage 5 ALZ BB99-887	25503	23.22	5674.88	11349.76	brain stage 5 ALZ	-1.04
brain stage 5 ALZ BB99-862	25504	23.5	4868.6	9737.20	brain stage 5 ALZ	-1.21
brain stage 5 ALZ BB99-927	25542	23.17	5843.2	11686.40	brain stage 5 ALZ	-1.01
CT lung	normal	25.61	1486.99	2973.98	CT lung Nml	
lung 26	normal	26.55	879.91		lung 26 Nml	
lung 27	normal	29.44	174.3	174.30	lung 27 Nml	

lung 24	COPD	29.99	128.5	128.50	lung 24 COPD	-8.67
lung 28	COPD	29.56	163.34	163.34	lung 28 COPD	-6.82
lung 23	COPD	29.59	160.67	160.67	lung 23 COPD	-6.94
lung 25	normal	29.24	194.83	194.83	lung 25 Nml	
asthmatic lung ODO3112	29321	27.22	604.38	604.38	asthmatic lung	-1.84
asthmatic lung ODO3433	29323	26.46	923.43	1846.86	asthmatic lung	1.66
asthmatic lung ODO3397	29322	26.16	1094.36	2188.72	asthmatic lung	1.96
asthmatic lung ODO4928	29325	25.51	1576.72	3153.44	asthmatic lung	2.83
endo cells	control	29.09	211.78	211.78	endo cells	
endo VEGF		30.07	122.67	122.67	endo VEGF	-1.73
endo bFGF		29.93	132.63	132.63	endo bFGF	-1.60
heart Clontech	normal	27.35	561.26	1122.52	heart	
heart (T-1) ischemic	29417	23.82	4053.65	8107.30	heart (T-1) ischemic	7.22
heart (T-14) non-obstructive DCM	29422	23.96	3746.25	7492.50	heart (T-14) non-obstructive DCM	6.67
heart (T-3399) DCM	29426	23.35	5282.35	10564.70	heart (T-3399) DCM	9.41
adenoid GW99-269	26162	25.71	1405.41	2810.82	adenoid	
tonsil GW98-280	22582	23.97	3725.77	7451.54	tonsil	
T cells PC00314	28453	25.03	2062.68	4125.36	T cells	
PBMNC		30.16	116.69	116.69	PBMNC	
monocyte		30.15	117.05	234.10	monocyte	
B cells PC00665	28455	23.22	5673.63	11347.26	B cells	
dendritic cells	28441	25.74	1385.65	2771.30	dendritic cells	
neutrophils	28440	27.14	631.86	631.86	neutrophils	
eosinophils	28446	28.27	335.66	671.32	eosinophils	
BM unstim		30.08	122.25	122.25	BM unstim	
BM stim	treated	29.57	162.71	162.71	BM stim	1.33
osteo dif	treated	29.07	214.84	214.84	osteo dif	2.91
osteo undif		30.98	73.85	73.85	osteo undif	
chondrocytes		25.41	1667.28	4168.20	chondrocytes	
OA Synovium IP12/01	29462	24.65	2554.39	2554.39	OA Synovium	
OA Synovium NP10/01	29461	25.72	1399	2798.00	OA Synovium	
OA Synovium NP57/00	28464	25.24	1828.2	3656.40	OA Synovium	
RA Synovium NP03/01	28466	25.69	1422.61	2845.22	RA Synovium	
RA Synovium NP71/00	28467	25.25	1818.15	3636.30	RA Synovium	
RA Synovium NP45/00	28475	25.22	1857.13	3714.26	RA Synovium	
OA bone (biobank)	29217	26.19	1074.74	1074.74	OA bone (biobank)	
OA bone Sample 1	J. Emory	26.71	805.65	1611.30	OA bone	
OA bone Sample 2	J. Emory	26.96	700.88	1401.76	OA bone	
Cartilage (pool)	Normal	26.38	968.45	1936.90	Nml Cartilage (pool)	
Cartilage (pool)	OA	28.07	376.23	752.46	OA Cartilage (pool)	-2.57
PBL uninfected	28441	25.09	1997.75	3995.50	PBL uninfected	
PBL HIV IIIB	28442	25.36	1710.81	3421.62	PBL HIV IIIB	-1.17
MRC5 uninfected (100%)	29158	25.28	1788.71	3577.42	MRC5 uninfected (100%)	

MRC5 HSV strain F	29178	30.17	116.17	232.34	MRC5 HSV strain F	-15.40
W12 cells	29179	27.6	489.01	978.02	W12 cells	
Keratinocytes	29180	26.4	959.61	1919.22	Keratinocytes	
B-actin control		25.62	1482.86			
genomic		25.42	1657.68			
1.00E+05		18.49	100000			
1.00E+05		18.49	100000			
1.00E+04		21.94	10000			
1.00E+04		21.98	10000			
1.00E+03		25.34	1000			
1.00E+03		25.39	1000			
1.00E+02		30.59	100			
1.00E+02		30.9	100			
1.00E+01		32.51	10			
1.00E+01		39.12	10			
1.00E-00		39.07	1			
1.00E-00		36.71	1			
NTC		39.63	-1			
*lung 26 Normal has been omitted due to multiple amplification failures from that sample						

Gene Name sbg1012732GLUT

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.08
colon tumor	1.69
colon tumor	1.00
colon tumor	1.31
lung tumor	-1.76
lung tumor	1.29
lung tumor	-1.28
lung tumor	1.18
breast tumor	2.49
breast tumor	2.23
breast tumor	2.45
breast tumor	-1.02
brain stage 5 ALZ	-2.38
brain stage 5 ALZ	-1.04
brain stage 5 ALZ	-1.21
brain stage 5 ALZ	-1.01
lung 24	-8.67
lung 28	-6.82
lung 23	-6.94
asthmatic lung	-1.84
asthmatic lung	1.66
asthmatic lung	1.96
asthmatic lung	2.83
endo VEGF	-1.73

endo bFGF	-1.60
heart T-1	7.22
heart T-14	6.67
heart T-3399	9.41
BM stim	1.33
osteo dif	2.91
Cartilage (pool)	-2.57
PBL HIV IIIB	-1.17
MRC5 HSV strain F	-15.40

Gene Name sbg1012732GLUTb

The same as sbg1012732GLUT.

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Gene Name sbg1018172CSP

Moderate to low overall expression. Highest normal expression is seen in the whole brain, kidney, thyroid, and uterus. This gene is expressed in all of the samples representing the female reproductive system. Highest disease expression is seen in many of the normal/tumor lung samples and the asthmatic lung samples. Downregulation in 2 of 4 lung tumor samples and upregulation in 2 of 4 breast tumor samples suggests an involvement in cancers of the lung and breast. Downregulation in 3 of 3 COPD samples suggests a potential role for this gene in chronic obstructive pulmonary disorder. Upregulation in 2 of 4 asthmatic lung samples implies an involvement in asthma. Upregulation in 1 of 3 disease heart samples implies an involvement in cardiovascular disease such as obstructive DCM. Downregulation in the OA cartilage pool with corroborating low expression in the immune cells (T and B cells in particular) implicates this gene in osteoarthritis and rheumatoid arthritis. Upregulation in the HSV-infected MRC5 cells suggests that this gene may be a host factor in HSV.

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Sample sbg1018172CSP	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	35.54, 34.87	7.65	11.21	9.43	3.06	16.34	154.08
Subcutaneous Adipose Zenbio	40, 40	0.4	0	0.20	0.96	52.36	10.47
Adrenal Gland Clontech	40, 40	0	0	0.00	0.61	81.97	0.00
Whole Brain Clontech	25.71, 25.78	1950.98	1867.58	1909.28	7.24	6.91	13185.6 4
Fetal Brain Clontech	40, 40	0	0	0.00	0.48	103.95	0.00
Cerebellum Clontech	36.32, 35.16	4.95	9.48	7.22	2.17	23.04	166.24
Cervix	36.76, 36.16	3.85	5.42	4.64	2.42	20.66	95.76
Colon	36.52, 36.41	4.41	4.7	4.56	2.71	18.45	84.04
Endometrium	36.4, 35.92	4.73	6.19	5.46	0.73	68.21	372.44
Esophagus	40, 40	0	0	0.00	1.37	36.50	0.00
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	40, 40	0	0	0.00	2.58	19.38	0.00
Jejunum	36.53, 33.22	4.38	28.28	16.33	6.60	7.58	123.71

Kidney	32.81, 32.45	35.74	43.67	39.71	2.12	23.58	936.44
Liver	35.92, 36.2	6.19	5.29	5.74	1.50	33.33	191.33
Fetal Liver Clontech	31.57, 30.46	71.69	134.34	103.02	10.40	4.81	495.26
Lung	33.35, 36.86	26.32	3.65	14.99	2.57	19.46	291.54
Mammary Gland Clontech	32.99, 32.17	32.23	51.27	41.75	13.00	3.85	160.58
Myometrium	34.99, 40	10.44	0	5.22	2.34	21.37	111.54
Omentum	35.61, 40	7.37	0	3.69	3.94	12.69	46.76
Ovary	35.83, 35.54	6.53	7.67	7.10	4.34	11.52	81.80
Pancreas	35.86, 40	6.39	0	3.20	0.81	61.80	197.47
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	34.26, 34.03	15.73	17.96	16.85	5.48	9.12	153.70
Placenta Clontech	32.64, 33.16	39.34	29.26	34.30	5.26	9.51	326.05
Prostate	35.71, 40	6.95	0	3.48	3.00	16.67	57.92
Rectum	33.84, 34.42	19.99	14.41	17.20	1.23	40.65	699.19
Salivary Gland Clontech	40, 40	0	0	0.00	7.31	6.84	0.00
Skeletal Muscle Clontech	34.2, 40	16.33	0	8.17	1.26	39.68	324.01
Skin	35.02, 40	10.31	0.48	5.40	1.21	41.32	222.93
Small Intestine Clontech	40, 40	0	0	0.29	0.98	51.07	14.81
Spleen	40, 35.31	0	8.71	4.36	4.92	10.16	44.26
Stomach	40, 35.4	0	8.3	4.15	2.73	18.32	76.01
Testis Clontech	40, 37.31	0	2.82	1.41	0.57	87.87	123.90
Thymus Clontech	30.9, 31.1	104.45	93.52	98.99	9.89	5.06	500.43
Thyroid	31.62, 31.57	69.89	71.93	70.91	2.77	18.05	1279.96
Trachea Clontech	34.19, 34.08	16.41	17.49	16.95	9.71	5.15	87.28
Urinary Bladder	40, 34.4	0	14.55	7.28	5.47	9.14	66.50
Uterus	30.63, 30.6	122.13	123.57	122.85	5.34	9.36	1150.28
genomic	26.58	1190.6					
b-actin	27.38	758.43					
1.00E+05	19.07	100000					
1.00E+05	19.35	100000					
1.00E+04	22.57	10000					
1.00E+04	22.59	10000					
1.00E+03	26.24	1000					
1.00E+03	26.31	1000					
1.00E+02	30.18	100					
1.00E+02	31.64	100					
1.00E+01	35.9	10					
1.00E+01	40	0					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	0					
NTC	40	0					

Sample	Reg number	Ct	Mean GOI	copies of mRNA	Sample	Fold Change
sbg1018172CSP						

	(GSK identifier)		copies	detected/ 50 ng total RNA		in Disease Populati on
colon normal GW98-167	21941	27.29	1064.89	2129.78	colon normal	
colon tumor GW98-166	21940	26.18	2023.11	4046.22	colon tumor	1.90
colon normal GW98-178	22080	30.45	168.68	337.36	colon normal	
colon tumor GW98-177	22060	29.33	324.49	648.98	colon tumor	1.92
colon normal GW98-561	23514	30.36	177.62	355.24	colon normal	
colon tumor GW98-560	23513	32.27	58.7	117.40	colon tumor	-3.03
colon normal GW98-894	24691	30.71	145.57	291.14	colon normal	
colon tumor GW98-893	24690	32.3	57.43	114.86	colon tumor	-2.53
lung normal GW98-3	20742	24.82	4478.67	8957.34	lung normal	
lung tumor GW98-2	20741	33.61	26.86	53.72	lung tumor	-166.74
lung normal GW97-179	20677	26.31	1874.25	3748.50	lung normal	
lung tumor GW97-178	20676	24.52	5311.72	10623.44	lung tumor	2.83
lung normal GW98-165	21922	24.99	4042.28	8084.56	lung normal	
lung tumor GW98-164	21921	27.19	1127.26	2254.52	lung tumor	-3.59
lung normal GW98-282	22584	25.51	2990.53	5981.06	lung normal	
lung tumor GW98-281	22583	26.67	1522.51	3045.02	lung tumor	-1.96
breast normal GW00-392	28750	32.25	59.17	59.17	breast normal	
breast tumor GW00-391	28746	30.48	165.82	331.64	breast tumor	5.60
breast normal GW00-413	28798	34.58	15.31	15.31	breast normal	
breast tumor GW00-412	28797	30.05	213.4	426.80	breast tumor	27.88
breast normal GW00-235:238	27592-95	34.41	16.85	16.85	breast normal	
breast tumor GW00-231:234	27588-91	33.52	28.31	28.31	breast tumor	1.68
breast normal GW98-621	23656	28.22	618.19	1236.38	breast normal	
breast tumor GW98-620	23655	32.02	67.94	135.88	breast tumor	-9.10
brain normal BB99-542	25507	29.11	367.88	735.76	brain normal	
brain normal BB99-406	25509	28.05	682.39	1364.78	brain normal	
brain normal BB99-904	25546	29.06	379.07	758.14	brain normal	
brain stage 5 ALZ BB99-874	25502	30.06	211.81	423.62	brain stage 5 ALZ	-2.25
brain stage 5 ALZ BB99-887	25503	26.97	1280.13	2560.26	brain stage 5 ALZ	2.69
brain stage 5 ALZ BB99-862	25504	29.85	239.03	478.06	brain stage 5 ALZ	-1.99
brain stage 5 ALZ BB99-927	25542	28.13	652.56	1305.12	brain stage 5 ALZ	1.37
CT lung	normal	26.97	1280.81	2561.62	CT lung Nml	
lung 26	normal	32.21	60.75		lung 26 Nml	
lung 27	normal	34	21.39	21.39	lung 27 Nml	
lung 24	COPD	32.11	64.11	64.11	lung 24 COPD	-13.87
lung 28	COPD	33.01	38.18	38.18	lung 28 COPD	-23.29
lung 23	COPD	32.84	42.15	42.15	lung 23 COPD	-21.10
lung 25	normal	31.63	84.78	84.78	lung 25 Nml	
asthmatic lung ODO3112	29321	29.4	310.75	310.75	asthmatic lung	-2.86
asthmatic lung ODO3433	29323	27.02	1242.79	2485.58	asthmatic lung	2.80

asthmatic lung ODO3397	29322	25.97	2289.74	4579.48	asthmatic lung	5.15
asthmatic lung ODO4928	29325	26.84	1380.5	2761.00	asthmatic lung	3.10
endo cells	control	40	0	0.00	endo cells	
endo VEGF		40	0	0.00	endo VEGF	0.00
endo bFGF		40	1.01	1.01	endo bFGF	1.01
heart Clontech	normal	33.02	37.93	75.86	heart	
heart (T-1) ischemic	29417	34.34	17.51	35.02	heart (T-1) ischemic	-2.17
heart (T-14) non- obstructive DCM	29422	34.85	13.07	26.14	heart (T-14) non- obstructive DCM	-2.90
heart (T-3399) DCM	29426	29.74	254.69	509.38	heart (T-3399) DCM	6.71
adenoid GW99-269	26162	35.07	11.5	23.00	adenoid	
tonsil GW98-280	22582	40	0	0.00	tonsil	
T cells PC00314	28453	36.12	6.22	12.44	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	40	0	0.00	B cells	
dendritic cells	28441	40	0	0.00	dendritic cells	
neutrophils	28440	35.43	9.3	9.30	neutrophils	
eosinophils	28446	40	1.32	2.64	eosinophils	
BM unstim		40	0	0.00	BM unstim	
BM stim	treated	40	0	0.00	BM stim	0.00
osteo dif	treated	40	0	0.00	osteo dif	0.00
osteo undif		40	0	0.00	osteo undif	
chondrocytes		33.23	33.49	83.73	chondrocytes	
OA Synovium IP12/01	29462	34.9	12.68	12.68	OA Synovium	
OA Synovium NP10/01	29461	28.55	510.63	1021.26	OA Synovium	
OA Synovium NP57/00	28464	34	21.41	42.82	OA Synovium	
RA Synovium NP03/01	28466	40	0	0.00	RA Synovium	
RA Synovium NP71/00	28467	36.2	5.96	11.92	RA Synovium	
RA Synovium NP45/00	28475	36.38	5.34	10.68	RA Synovium	
OA bone (biobank)	29217	35.58	8.52	8.52	OA bone (biobank)	
OA bone Sample 1	J. Emory	33.54	27.91	55.82	OA bone	
OA bone Sample 2	J. Emory	34.92	12.54	25.08	OA bone	
Cartilage (pool)	Normal	33.88	22.98	45.96	Nml Cartilage (pool)	
Cartilage (pool)	OA	40	0	0.00	OA Cartilage (pool)	-45.96
PBL uninfected	28441	30.74	142.65	285.30	PBL uninfected	
PBL HIV IIIB	28442	32.47	52.13	104.26	PBL HIV IIIB	-2.74
MRC5 uninfected (100%)	29158	40	0	0.00	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	30.06	211.88	423.76	MRC5 HSV strain F	423.76
W12 cells	29179	39.65	0.8	1.60	W12 cells	
Keratinocytes	29180	33.76	24.58	49.16	Keratinocytes	
B-actin control		27.17	1140.82			
genomic		26.81	1405.46			

1.00E+05		19.68	100000			
1.00E+05		19.63	100000			
1.00E+04		23.15	10000			
1.00E+04		23.27	10000			
1.00E+03		27.1	1000			
1.00E+03		27.33	1000			
1.00E+02		31.34	100			
1.00E+02		32.04	100			
1.00E+01		35.09	10			
1.00E+01		40	10			
1.00E-00		40	0			
1.00E-00		40	0			
NTC		40	0			
*lung 26 Normal has been omitted due to multiple amplification failures from that sample						

Gene Name sbg1018172CSP

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	1.90
colon tumor	1.92
colon tumor	-3.03
colon tumor	-2.53
lung tumor	-166.74
lung tumor	2.83
lung tumor	-3.59
lung tumor	-1.96
breast tumor	5.60
breast tumor	27.88
breast tumor	1.68
breast tumor	-9.10
brain stage 5 ALZ	-2.25
brain stage 5 ALZ	2.69
brain stage 5 ALZ	-1.99
brain stage 5 ALZ	1.37
lung 24	-13.87
lung 28	-23.29
lung 23	-21.10
asthmatic lung	-2.86
asthmatic lung	2.80
asthmatic lung	5.15
asthmatic lung	3.10
endo VEGF	0.00
endo bFGF	1.01
heart T-1	-2.17
heart T-14	-2.90
heart T-3399	6.71
BM stim	0.00
osteo dif	0.00
Cartilage (pool)	-45.96

PBL HIV IIIB	-2.74
MRC5 HSV strain F	423.76

Gene Name sbg1004570ERGIC

5 Moderate to low overall expression. This gene is expressed fairly ubiquitously in all normal samples analyzed with highest levels of expression seen in the whole brain, hypothalamus, pancreas, and head of pancreas. This pattern of expression suggests that this gene may be involved in diabetes or other metabolic diseases. Highest disease expression is seen in the colon, breast, and lung normal/tumor pairs as well as the Alzheimer's brain samples and the T cells, B cells, dendritic cells, and eosinophils. Upregulation in 2 of 4 breast tumor samples suggests a role for this gene in breast cancer. Upregulation in 2 of 4 Alzheimer's brain samples implies an involvement in
10 Alzheimer's disease. Downregulation in 3 of 3 COPD samples and 4 of 4 asthmatic lung samples suggests a potential role for this gene in chronic obstructive pulmonary disorder and asthma. Upregulated in the stimulated bone marrow sample.

Sample sbg1004570ERGIC	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected/50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 40	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	39.46, 35.22	0.08	1.37	0.73	0.96	52.36	37.96
Adrenal Gland Clontech	36.91, 36.21	0.43	0.7	0.57	0.61	81.97	46.31
Whole Brain Clontech	26.46, 30.31	547.02	39.49	293.26	7.24	6.91	2025.24
Fetal Brain Clontech	36.04, 36.66	0.78	0.51	0.65	0.48	103.95	67.05
Cerebellum Clontech	35.46, 34.63	1.16	2.06	1.61	2.17	23.04	37.10
Cervix	35.63, 36.28	1.04	0.67	0.86	2.42	20.66	17.67
Colon	35.38, 34.57	1.23	2.13	1.68	2.71	18.45	31.00
Endometrium	40, 35.24	0.06	1.35	0.71	0.73	68.21	48.09
Esophagus	35.02, 36.31	1.57	0.65	1.11	1.37	36.50	40.51
Heart Clontech	37.16, 35.48	0.36	1.15	0.76	1.32	37.88	28.60
Hypothalamus	35.15, 36.01	1.44	0.8	1.12	0.32	155.28	173.91
Ileum	35.04, 35.5	1.55	1.13	1.34	2.58	19.38	25.97
Jejunum	35.14, 34.88	1.45	1.73	1.59	6.60	7.58	12.05
Kidney	35.81, 37.16	0.91	0.36	0.64	2.12	23.58	14.98
Liver	36.19, 34.39	0.71	2.42	1.57	1.50	33.33	52.17
Fetal Liver Clontech	32.94, 33.1	6.51	5.85	6.18	10.40	4.81	29.71
Lung	34.54, 35.16	2.18	1.43	1.81	2.57	19.46	35.12
Mammary Gland Clontech	34.45, 34.76	2.33	1.88	2.11	13.00	3.85	8.10
Myometrium	34.08, 34.61	2.98	2.09	2.54	2.34	21.37	54.17
Omentum	35.22, 36.18	1.37	0.71	1.04	3.94	12.69	13.20
Ovary	34.52, 34.83	2.21	1.78	2.00	4.34	11.52	22.98
Pancreas	34.45, 33.99	2.32	3.18	2.75	0.81	61.80	169.96
Head of Pancreas	33.24, 33.63	5.32	4.06	4.69	1.57	31.85	149.36
Parotid Gland	33.22, 33.08	5.38	5.9	5.64	5.48	9.12	51.46
Placenta Clontech	36.02, 35.39	0.79	1.22	1.01	5.26	9.51	9.55

Prostate	35.98, 35.07	0.81	1.51	1.16	3.00	16.67	19.33
Rectum	36.71, 37.13	0.49	0.37	0.43	1.23	40.65	17.48
Salivary Gland Clontech	33.51, 34.22	4.41	2.71	3.56	7.31	6.84	24.35
Skeletal Muscle Clontech	35.53, 34.52	1.11	2.21	1.66	1.26	39.68	65.87
Skin	36.02, 36.07	0.79	0.77	0.78	1.21	41.32	32.23
Small Intestine Clontech	35.02, 37.21	1.57	0.35	0.96	0.98	51.07	49.03
Spleen	35.64, 35.27	1.03	1.33	1.18	4.92	10.16	11.99
Stomach	35.08, 35.41	1.51	1.2	1.36	2.73	18.32	24.82
Testis Clontech	35.48, 38.1	1.15	0.19	0.67	0.57	87.87	58.88
Thymus Clontech	32.15, 31.72	11.16	14.98	13.07	9.89	5.06	66.08
Thyroid	35.61, 35.09	1.05	1.49	1.27	2.77	18.05	22.92
Trachea Clontech	35.04, 34.75	1.55	1.89	1.72	9.71	5.15	8.86
Urinary Bladder	36.11, 36.24	0.74	0.68	0.71	5.47	9.14	6.49
Uterus	35.59, 35.68	1.06	1	1.03	5.34	9.36	9.64
genomic	24.29	2416.83					
b-actin	26.09	706.6					
1.00E+05	20.09	100000					
1.00E+05	19.53	100000					
1.00E+04	21.72	10000					
1.00E+04	21.68	10000					
1.00E+03	24.13	1000					
1.00E+03	24.18	1000					
1.00E+02	29.13	100					
1.00E+02	30.16	100					
1.00E+01	31.7	10					
1.00E+01	33.16	10					
1.00E-00	36.93	1					
1.00E-00	34.75	1					
NTC	36	-1					
NTC	35.85	-1					

Sample sbg1004570ERGIC	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detecte d/50 ng total RNA	Sample	Fold Change in Disease Populati on
colon normal GW98-167	21941	30.51	38.25	76.50	colon normal	
colon tumor GW98-166	21940	31.28	23.13	46.26	colon tumor	-1.65
colon normal GW98-178	22080	31.79	16.57	33.14	colon normal	
colon tumor GW98-177	22060	31.3	22.86	45.72	colon tumor	1.38
colon normal GW98-561	23514	30.71	33.5	67.00	colon normal	
colon tumor GW98-560	23513	31.18	24.73	49.46	colon tumor	-1.35
colon normal GW98-894	24691	30.16	48.2	96.40	colon normal	
colon tumor GW98-893	24690	29.96	55	110.00	colon tumor	1.14
lung normal GW98-3	20742	30.1	50.19	100.38	lung normal	
lung tumor GW98-2	20741	32.86	8.15	16.30	lung tumor	-6.16

lung normal GW97-179	20677	31.65	18.14	36.28	lung normal	
lung tumor GW97-178	20676	31.05	26.89	53.78	lung tumor	1.48
lung normal GW98-165	21922	30.44	40.16	80.32	lung normal	
lung tumor GW98-164	21921	30.72	33.36	66.72	lung tumor	-1.20
lung normal GW98-282	22584	31.83	16.13	32.26	lung normal	
lung tumor GW98-281	22583	32.09	13.61	27.22	lung tumor	-1.19
breast normal GW00-392	28750	32.76	8.73	8.73	breast normal	
breast tumor GW00-391	28746	30.68	34.38	68.76	breast tumor	7.88
breast normal GW00-413	28798	37.11	0.5	0.50	breast normal	
breast tumor GW00-412	28797	30.8	31.72	63.44	breast tumor	126.88
breast normal GW00-235:238	27592-95	38.8	0.17	0.17	breast normal	
breast tumor GW00-231:234	27588-91	37.36	0.43	0.43	breast tumor	2.53
breast normal GW98-621	23656	31.67	17.86	35.72	breast normal	
breast tumor GW98-620	23655	32.59	9.8	19.60	breast tumor	-1.82
brain normal BB99-542	25507	33.66	4.83	9.66	brain normal	
brain normal BB99-406	25509	33.24	6.37	12.74	brain normal	
brain normal BB99-904	25546	33.2	6.54	13.08	brain normal	
brain stage 5 ALZ BB99-874	25502	33.1	6.97	13.94	brain stage 5 ALZ	1.18
brain stage 5 ALZ BB99-887	25503	30.93	29.17	58.34	brain stage 5 ALZ	4.93
brain stage 5 ALZ BB99-862	25504	31.44	20.73	41.46	brain stage 5 ALZ	3.51
brain stage 5 ALZ BB99-927	25542	32.93	7.83	15.66	brain stage 5 ALZ	1.32
CT lung	normal	32.62	9.6	19.20	CT lung Nml	
lung 26	normal				lung 26 Nml	
lung 27	normal	40	0	0.00	lung 27 Nml	
lung 24	COPD	39.15	0.13	0.13	lung 24 COPD	-49.46
lung 28	COPD	40	0.08	0.08	lung 28 COPD	-80.38
lung 23	COPD	38.59	0.19	0.19	lung 23 COPD	-33.84
lung 25	normal	40	0.09	0.09	lung 25 Nml	
asthmatic lung ODO3112	29321	40	0	0.00	asthmatic lung	-6.43
asthmatic lung ODO3433	29323	38.47	0.2	0.40	asthmatic lung	-16.08
asthmatic lung ODO3397	29322	38.01	0.28	0.56	asthmatic lung	-11.48
asthmatic lung ODO4928	29325	38.13	0.26	0.52	asthmatic lung	-12.37
endo cells	control	36.24	0.89	0.89	endo cells	
endo VEGF		39.8	0.09	0.09	endo VEGF	-9.89
endo bFGF		37.19	0.47	0.47	endo bFGF	-1.89
heart Clontech	normal	35.52	1.43	2.86	heart	
heart (T-1) ischemic	29417	33.79	4.43	8.86	heart (T-1) ischemic	3.10
heart (T-14) non-obstructive DCM	29422	34.81	2.27	4.54	heart (T-14) non-obstructive DCM	1.59
heart (T-3399) DCM	29426	34.11	3.59	7.18	heart (T-3399) DCM	2.51
adenoid GW99-269	26162	34.97	2.05	4.10	adenoid	
tonsil GW98-280	22582	33.05	7.23	14.46	tonsil	

T cells PC00314	28453	31.09	26.2	52.40	T cells	
PBMNC		38.01	0.28	0.28	PBMNC	
monocyte		36.29	0.86	1.72	monocyte	
B cells PC00665	28455	32.13	13.23	26.46	B cells	
dendritic cells	28441	31.94	14.96	29.92	dendritic cells	
neutrophils	28440	34.08	3.66	3.66	neutrophils	
eosinophils	28446	32.23	12.37	24.74	eosinophils	
BM unstim		39.73	0.09	0.09	BM unstim	
BM stim	treated	37.03	0.53	0.53	BM stim	5.89
osteo dif	treated	36.8	0.61	0.61	osteo dif	0.61
osteo undif		40	0	0.00	osteo undif	
chondrocytes		31.85	15.9	39.75	chondrocytes	
OA Synovium IP12/01	29462	38.61	0.19	0.19	OA Synovium	
OA Synovium NP10/01	29461	33.11	6.96	13.92	OA Synovium	
OA Synovium NP57/00	28464	33.81	4.39	8.78	OA Synovium	
RA Synovium NP03/01	28466	33.11	6.96	13.92	RA Synovium	
RA Synovium NP71/00	28467	32.03	14.14	28.28	RA Synovium	
RA Synovium NP45/00	28475	32.47	10.55	21.10	RA Synovium	
OA bone (biobank)	29217	35.25	1.7	1.70	OA bone (biobank)	
OA bone Sample 1	J. Emory	34.54	2.72	5.44	OA bone	
OA bone Sample 2	J. Emory	36.28	0.87	1.74	OA bone	
Cartilage (pool)	Normal	35.24	1.71	3.42	Nml Cartilage (pool)	
Cartilage (pool)	OA	34.45	2.87	5.74	OA Cartilage (pool)	1.68
PBL uninfected	28441	32.53	10.19	20.38	PBL uninfected	
PBL HIV IIIB	28442	31.77	16.79	33.58	PBL HIV IIIB	1.65
MRC5 uninfected (100%)	29158	33.12	6.87	13.74	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	33.76	4.54	9.08	MRC5 HSV strain F	-1.51
W12 cells	29179	33.1	6.96	13.92	W12 cells	
Keratinocytes	29180	32.67	9.29	18.58	Keratinocytes	
B-actin control		26.03	726.55			
genomic		24.63	1825.58			
1.00E+05		19.96	100000			
1.00E+05		19.27	100000			
1.00E+04		21.83	10000			
1.00E+04		21.45	10000			
1.00E+03		23.86	1000			
1.00E+03		23.84	1000			
1.00E+02		28.42	100			
1.00E+02		29.35	100			
1.00E+01		33.3	10			
1.00E+01		35.09	10			
1.00E-00		35.16	1			
1.00E-00		36.05	1			
NTC		38.24	-1			
*lung 26 Normal has						

been omitted due to multiple amplification failures from that sample						
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Gene Name sbg1004570ERGIC

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-1.65
colon tumor	1.38
colon tumor	-1.35
colon tumor	1.14
lung tumor	-6.16
lung tumor	1.48
lung tumor	-1.20
lung tumor	-1.19
breast tumor	7.88
breast tumor	126.88
breast tumor	2.53
breast tumor	-1.82
brain stage 5 ALZ	1.18
brain stage 5 ALZ	4.93
brain stage 5 ALZ	3.51
brain stage 5 ALZ	1.32
lung 24	-49.46
lung 28	-80.38
lung 23	-33.84
asthmatic lung	-6.43
asthmatic lung	-16.08
asthmatic lung	-11.48
asthmatic lung	-12.37
endo VEGF	-9.89
endo bFGF	-1.89
heart T-1	3.10
heart T-14	1.59
heart T-3399	2.51
BM stim	5.89
osteo dif	0.61
Cartilage (pool)	1.68
PBL HIV IIIB	1.65
MRC5 HSV strain F	-1.51

Gene Name sbg1016995IGBrcpt

- 5 Moderate to low overall expression. Highest normal expression is seen in the whole brain in lung with slightly lower levels of expression in the endometrium, ileum, rectum, and skin. High level of expression in the skin may suggest a possible role for this gene in psoriasis and Lupus. The patterns of expression in the samples on the disease plate indicate that this gene is highly specific to the adenoid and tonsil. Downregulation in 2 of 4 lung tumor samples and upregulation in 2 of 4 breast tumor samples suggests an involvement in cancers of the lung and breast.
- 10 Downregulation in 3 of 3 COPD samples suggests a potential role for this gene in chronic obstructive pulmonary disorder. Upregulated in the stimulated bone marrow sample. Downregulated in the differentiated osteoblast. Upregulated in the HIV-infected PBL cells suggests that this gene may be a host factor in HIV.

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Sample	Ct (sample	Mean	Mean	Average	18S	50	copies of
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sbg1016995IGBrectp	1 and 2)	GOI copies (sample 1)	GOI copies (sample 2)	GOI Copies	rRNA (ng)	ng/18S rRNA (ng)	mRNA detected/ 50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 40	0.61	0.61	0.61	3.06	16.34	9.97
Subcutaneous Adipose Zenbio	40, 40	0.59	0.56	0.58	0.96	52.36	30.10
Adrenal Gland Clontech	39.89, 39.79	0.54	0.57	0.56	0.61	81.97	45.49
Whole Brain Clontech	30.69, 30.76	108.67	104.35	106.51	7.24	6.91	735.57
Fetal Brain Clontech	39.41, 40	0.71	0.62	0.67	0.48	103.95	69.13
Cerebellum Clontech	39.33, 37.82	0.74	1.78	1.26	2.17	23.04	29.03
Cervix	36.12, 36.58	4.73	3.62	4.18	2.42	20.66	86.26
Colon	35.23, 38.35	7.9	1.31	4.61	2.71	18.45	84.96
Endometrium	35.51, 40	6.73	0	3.37	0.73	68.21	229.54
Esophagus	37.22, 38.18	2.5	1.45	1.98	1.37	36.50	72.08
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	34.65, 34.11	11.04	15.09	13.07	2.58	19.38	253.20
Jejunum	34.84, 34.04	9.91	15.72	12.82	6.60	7.58	97.08
Kidney	38.2, 39.11	1.43	0.84	1.14	2.12	23.58	26.77
Liver	34.47, 38.59	12.26	1.14	6.70	1.50	33.33	223.33
Fetal Liver Clontech	33.51, 33.07	21.26	27.43	24.35	10.40	4.81	117.04
Lung	27.32, 37.11	755.31	2.68	379.00	2.57	19.46	7373.44
Mammary Gland Clontech	36.31, 36.4	4.24	4.03	4.14	13.00	3.85	15.90
Myometrium	40, 38.7	0.7	1.07	0.89	2.34	21.37	18.91
Omentum	35.44, 36.14	6.98	4.68	5.83	3.94	12.69	73.98
Ovary	38.76, 35.49	1.03	6.82	3.93	4.34	11.52	45.22
Pancreas	40, 38.56	0.48	1.16	0.82	0.81	61.80	50.68
Head of Pancreas	40, 40	0	0	0.00	1.57	31.85	0.00
Parotid Gland	36.8, 35.45	3.2	6.98	5.09	5.48	9.12	46.44
Placenta Clontech	35.63, 35.11	6.27	8.47	7.37	5.26	9.51	70.06
Prostate	37.4, 37.5	2.26	2.14	2.20	3.00	16.67	36.67
Rectum	35.45, 35.25	6.94	7.81	7.38	1.23	40.65	299.80
Salivary Gland Clontech	37.3, 37.06	2.4	2.75	2.58	7.31	6.84	17.61
Skeletal Muscle Clontech	40, 39.34	0	0.74	0.37	1.26	39.68	14.68
Skin	38.84, 34.56	0.98	11.63	6.31	1.21	41.32	260.54
Small Intestine Clontech	40, 40	0	0.63	0.32	0.98	51.07	16.09
Spleen	34.37, 34.89	13	9.6	11.30	4.92	10.16	114.84
Stomach	39.73, 35.52	0.59	6.67	3.63	2.73	18.32	66.48
Testis Clontech	38.91, 40	0.94	0	0.47	0.57	87.87	41.30
Thymus Clontech	31.96, 32.96	52.16	29.2	40.68	9.89	5.06	205.66
Thyroid	35.53, 40	6.66	0	3.33	2.77	18.05	60.11
Trachea Clontech	37.99, 37.69	1.61	1.91	1.76	9.71	5.15	9.06

Urinary Bladder	39.69, 39.02	0.6	0.89	0.75	5.47	9.14	6.81
Uterus	34.41, 33.56	12.67	20.75	16.71	5.34	9.36	156.46
genomic	26.31	1359.1					
b-actin	27.2	812.88					
1.00E+05	19.24	100000					
1.00E+05	19.38	100000					
1.00E+04	22.67	10000					
1.00E+04	22.67	10000					
1.00E+03	26.31	1000					
1.00E+03	26.28	1000					
1.00E+02	30.17	100					
1.00E+02	31.02	100					
1.00E+01	36.17	10					
1.00E+01	34.46	10					
1.00E-00	40	0					
1.00E-00	40	1					
NTC	40	-1					
NTC	40	-1					

Sample sbg1016995IGBrecpt	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detecte d/50 ng total RNA	Sample	Fold Change in Disease Populati on
colon normal GW98-167	21941	29.45	174.86	349.72	colon normal	
colon tumor GW98-166	21940	32.1	33.44	66.88	colon tumor	-5.23
colon normal GW98-178	22080	31.77	41.07	82.14	colon normal	
colon tumor GW98-177	22060	32.66	23.5	47.00	colon tumor	-1.75
colon normal GW98-561	23514	29.15	211.24	422.48	colon normal	
colon tumor GW98-560	23513	31.25	56.95	113.90	colon tumor	-3.71
colon normal GW98-894	24691	30.68	81.3	162.60	colon normal	
colon tumor GW98-893	24690	31.33	54.12	108.24	colon tumor	-1.50
lung normal GW98-3	20742	31.86	38.92	77.84	lung normal	
lung tumor GW98-2	20741	34.55	7.25	14.50	lung tumor	-5.37
lung normal GW97-179	20677	28.38	342.07	684.14	lung normal	
lung tumor GW97-178	20676	32.1	33.52	67.04	lung tumor	-10.20
lung normal GW98-165	21922	32.2	31.46	62.92	lung normal	
lung tumor GW98-164	21921	30.5	90.8	181.60	lung tumor	2.89
lung normal GW98-282	22584	29.82	138.8	277.60	lung normal	
lung tumor GW98-281	22583	32.72	22.64	45.28	lung tumor	-6.13
breast normal GW00-392	28750	31.5	48.65	48.65	breast normal	
breast tumor GW00-391	28746	31.9	37.84	75.68	breast tumor	1.56
breast normal GW00-413	28798	34.37	8.07	8.07	breast normal	
breast tumor GW00-412	28797	29.97	126.73	253.46	breast tumor	31.41
breast normal GW00-	27592-95	35.08	5.2	5.20	breast normal	

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breast tumor GW00-231:234	27588-91	32.3	29.54	29.54	breast tumor	5.68
breast normal GW98-621	23656	31.11	61.96	123.92	breast normal	
breast tumor GW98-620	23655	31.27	56.22	112.44	breast tumor	-1.10
brain normal BB99-542	25507	33.3	15.82	31.64	brain normal	
brain normal BB99-406	25509	33.02	18.83	37.66	brain normal	
brain normal BB99-904	25546	33.93	10.62	21.24	brain normal	
brain stage 5 ALZ BB99-874	25502	32.36	28.38	56.76	brain stage 5 ALZ	1.88
brain stage 5 ALZ BB99-887	25503	31.79	40.66	81.32	brain stage 5 ALZ	2.69
brain stage 5 ALZ BB99-862	25504	32.04	34.76	69.52	brain stage 5 ALZ	2.30
brain stage 5 ALZ BB99-927	25542	31.79	40.51	81.02	brain stage 5 ALZ	2.68
CT lung	normal	33.32	15.63	31.26	CT lung Nml	
lung 26	normal	29.8	140.4		lung 26 Nml	
lung 27	normal	38.71	0.54	0.54	lung 27 Nml	
lung 24	COPD	39.31	0.37	0.37	lung 24 COPD	-29.00
lung 28	COPD	37.09	1.48	1.48	lung 28 COPD	-7.25
lung 23	COPD	38.02	0.83	0.83	lung 23 COPD	-12.93
lung 25	normal	39.22	0.39	0.39	lung 25 Nml	
asthmatic lung ODO3112	29321	37.96	0.86	0.86	asthmatic lung	-12.48
asthmatic lung ODO3433	29323	31.15	60.54	121.08	asthmatic lung	11.28
asthmatic lung ODO3397	29322	33.74	12.01	24.02	asthmatic lung	2.24
asthmatic lung ODO4928	29325	31.59	46.09	92.18	asthmatic lung	8.59
endo cells	control	36.98	1.58	1.58	endo cells	
endo VEGF		39.28	0.38	0.38	endo VEGF	-4.16
endo bFGF		37.3	1.3	1.30	endo bFGF	-1.22
heart Clontech	normal	35.73	3.45	6.90	heart	
heart (T-1) ischemic	29417	34.7	6.58	13.16	heart (T-1) ischemic	1.91
heart (T-14) non-obstructive DCM	29422	37.5	1.15	2.30	heart (T-14) non-obstructive DCM	-3.00
heart (T-3399) DCM	29426	35.15	4.96	9.92	heart (T-3399) DCM	1.44
adenoid GW99-269	26162	25.98	1528.07	3056.14	adenoid	
tonsil GW98-280	22582	24.6	3626.43	7252.86	tonsil	
T cells PC00314	28453	34.49	7.5	15.00	T cells	
PBMNC		37.58	1.09	1.09	PBMNC	
monocyte		37.4	1.22	2.44	monocyte	
B cells PC00665	28455	31.68	43.59	87.18	B cells	
dendritic cells	28441	35.05	5.28	10.56	dendritic cells	
neutrophils	28440	35.68	3.57	3.57	neutrophils	
eosinophils	28446	35.07	5.23	10.46	eosinophils	
BM unstim		38.19	0.75	0.75	BM unstim	
BM stim	treated	34.27	8.61	8.61	BM stim	11.48
osteo dif	treated	40	0.09	0.09	osteo dif	-5.78
osteo undif		40	0.52	0.52	osteo undif	

chondrocytes		32.86	20.79	51.98	chondrocytes	
OA Synovium IP12/01	29462	31.85	38.99	38.99	OA Synovium	
OA Synovium NP10/01	29461	34.76	6.33	12.66	OA Synovium	
OA Synovium NP57/00	28464	31.39	51.96	103.92	OA Synovium	
RA Synovium NP03/01	28466	31.1	62.3	124.60	RA Synovium	
RA Synovium NP71/00	28467	31.95	36.76	73.52	RA Synovium	
RA Synovium NP45/00	28475	32.43	27.14	54.28	RA Synovium	
OA bone (biobank)	29217	35.84	3.22	3.22	OA bone (biobank)	
OA bone Sample 1	J. Emory	35.43	4.18	8.36	OA bone	
OA bone Sample 2	J. Emory	34.86	5.95	11.90	OA bone	
Cartilage (pool)	Normal	34.79	6.21	12.42	Nml Cartilage (pool)	
Cartilage (pool)	OA	36.55	2.07	4.14	OA Cartilage (pool)	-3.00
PBL uninfected	28441	30.02	122.76	245.52	PBL uninfected	
PBL HIV IIIB	28442	28.17	388.59	777.18	PBL HIV IIIB	3.17
MRC5 uninfected (100%)	29158	34.6	7.01	14.02	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	33.27	16.13	32.26	MRC5 HSV strain F	2.30
W12 cells	29179	34.43	7.8	15.60	W12 cells	
Keratinocytes	29180	35.04	5.31	10.62	Keratinocytes	
B-actin control		27	808.77			
genomic		26.18	1353.11			
1.00E+05		19.37	100000			
1.00E+05		19.59	100000			
1.00E+04		22.75	10000			
1.00E+04		22.8	10000			
1.00E+03		26.43	1000			
1.00E+03		26.17	1000			
1.00E+02		30.09	100			
1.00E+02		30.21	100			
1.00E+01		35.27	10			
1.00E+01		35.55	10			
1.00E-00		39.31	1			
1.00E-00		34.53	1			
NTC		40	-1			
*lung 26 Normal has been omitted due to multiple amplification failures from that sample						

Gene Name sbg1016995IGBrecpt

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	-5.23
colon tumor	-1.75
colon tumor	-3.71
colon tumor	-1.50

lung tumor	-5.37
lung tumor	-10.20
lung tumor	2.89
lung tumor	-6.13
breast tumor	1.56
breast tumor	31.41
breast tumor	5.68
breast tumor	-1.10
brain stage 5 ALZ	1.88
brain stage 5 ALZ	2.69
brain stage 5 ALZ	2.30
brain stage 5 ALZ	2.68
lung 24	-29.00
lung 28	-7.25
lung 23	-12.93
asthmatic lung	-12.48
asthmatic lung	11.28
asthmatic lung	2.24
asthmatic lung	8.59
endo VEGF	-4.16
endo bFGF	-1.22
heart T-1	1.91
heart T-14	-3.00
heart T-3399	1.44
BM stim	11.48
osteo dif	-5.78
Cartilage (pool)	-3.00
PBL HIV IIIB	3.17
MRC5 HSV strain F	2.30

Gene Name sbg1151bSREC

Highest overall expression in normal and disease samples. Fairly ubiquitously expressed but highest normal expression in adipocytes, adipose, whole brain, fetal brain, and endometrium. Highest disease expression in one of the colon tumor samples, one of the normal lung samples, chondrocytes, and the uninfected MRC5. There are no significant changes in brains from patients with Alzheimer's disease. Downregulation in 1 of 4 lung tumors suggests possible implication in lung cancer. Upregulation in 1 of 4 breast tumor samples is sufficient to claim a role in cancer of the breast. Upregulation in 1 of 4 asthma lungs implies a role in asthma. Downregulation in HSV implicates involvement in herpes simplex virus as a potential host factor. High expression in immune cells. High expression in cartilage and bone samples from patients with OA as well as high expression in chondrocytes possible involvement in osteoarthritis and rheumatoid arthritis. Additionally, the corroborating expression in immune cells (particularly B and T cells) provides additional evidence for a role in RA/OA.

Sample sbg1151bSREC	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detected /50 ng total RNA
Subcutaneous Adipocytes Zenbio	28.31, 28.35	477.04	466.02	471.53	3.06	16.34	7704.74
Subcutaneous Adipose Zenbio	30.79, 30.22	122.3	166.95	144.63	0.96	52.36	7571.99
Adrenal Gland Clontech	33.96, 33.47	21.39	27.97	24.68	0.61	81.97	2022.95
Whole Brain Clontech	24.07, 23.98	4889.28	5123.8	5006.54	7.24	6.91	34575.55

Fetal Brain Clontech	31.1, 32.29	103.16	53.55	78.36	0.48	103.95	8145.01
Cerebellum Clontech	31.03, 31.99	107.02	63.18	85.10	2.17	23.04	1960.83
Cervix	31.22, 30.06	96.6	182.64	139.62	2.42	20.66	2884.71
Colon	30.68, 30.53	129.52	140.99	135.26	2.71	18.45	2495.48
Endometrium	30.59, 30.44	136.06	147.8	141.93	0.73	68.21	9681.45
Esophagus	33.11, 32.17	34.08	57.32	45.70	1.37	36.50	1667.88
Heart Clontech	33.19, 32.41	32.68	50.11	41.40	1.32	37.88	1567.99
Hypothalamus	34.34, 40	17.4	0	8.70	0.32	155.28	1350.93
Ileum	31.29, 30.13	92.84	174.99	133.92	2.58	19.38	2595.25
Jejunum	29.7, 29.48	221.9	251.05	236.48	6.60	7.58	1791.48
Kidney	31.03, 30.17	107.15	171.45	139.30	2.12	23.58	3285.38
Liver	32.89, 33.16	38.61	33.17	35.89	1.50	33.33	1196.33
Fetal Liver Clontech	28.05, 28.15	550.64	518.95	534.80	10.40	4.81	2571.13
Lung	29.39, 28.63	263.85	398.99	331.42	2.57	19.46	6447.86
Mammary Gland Clontech	27.56, 27.39	717.67	789.94	753.81	13.00	3.85	2899.25
Myometrium	29.08, 28.93	312.86	339.46	326.16	2.34	21.37	6969.23
Omentum	30.72, 29.32	126.7	273.04	199.87	3.94	12.69	2536.42
Ovary	28.89, 28.68	346.91	388.02	367.47	4.34	11.52	4233.47
Pancreas	35.24, 35.75	10.59	8.02	9.31	0.81	61.80	575.09
Head of Pancreas	35.25, 33.21	10.57	32.34	21.46	1.57	31.85	683.28
Parotid Gland	28.46, 27.84	438.62	615.36	526.99	5.48	9.12	4808.30
Placenta Clontech	28.67, 28.66	391.9	393.15	392.53	5.26	9.51	3731.23
Prostate	30.55, 31.46	139.05	84.64	111.85	3.00	16.67	1864.08
Rectum	31.28, 31.43	93.33	85.92	89.63	1.23	40.65	3643.29
Salivary Gland Clontech	31.13, 30.57	101.46	138.16	119.81	7.31	6.84	819.49
Skeletal Muscle Clontech	34.05, 35.24	20.38	10.59	15.49	1.26	39.68	614.48
Skin	31.53, 31.2	81.49	97.36	89.43	1.21	41.32	3695.25
Small Intestine Clontech	34.81, 33.82	13.41	23.18	18.30	0.98	51.07	934.37
Spleen	31.01, 30.44	108.41	147.9	128.16	4.92	10.16	1302.39
Stomach	32.01, 31.1	62.6	102.97	82.79	2.73	18.32	1516.21
Testis Clontech	31.74, 32.29	72.49	53.45	62.97	0.57	87.87	5533.39
Thymus Clontech	28.84, 28.53	356.64	421.44	389.04	9.89	5.06	1966.84
Thyroid	30.12, 30.04	176.76	184.5	180.63	2.77	18.05	3260.47
Trachea Clontech	28.48, 28.38	434.3	459.42	446.86	9.71	5.15	2301.03
Urinary Bladder	29.63, 29.55	230.25	241.15	235.70	5.47	9.14	2154.48
Uterus	28.69, 28.37	387.47	461.07	424.27	5.34	9.36	3972.57
genomic	26.24	1487.44					
b-actin	27.28	839.2					
1.00E+05	18.96	100000					
1.00E+05	19.34	100000					
1.00E+04	22.64	10000					
1.00E+04	22.84	10000					
1.00E+03	26.22	1000					
1.00E+03	26.04	1000					
1.00E+02	31.04	100					

1.00E+02	30.1	100					
1.00E+01	33.33	10					
1.00E+01	39.08	10					
1.00E-00	40	0					
1.00E-00	40	1					
NTC	40	0					
NTC	40	0					

Sample sbg1151bSREC	Reg number (GSK identifie r)	Ct	Mean GOI copies	copies of mRNA detected /50 ng total RNA	Sample	Fold Change in Disease Populatio n
colon normal GW98-167	21941	24.55	5357.25	10714.50	colon normal	
colon tumor GW98-166	21940	22.61	19769.94	39539.88	colon tumor	3.69
colon normal GW98-178	22080	26.71	1252.3	2504.60	colon normal	
colon tumor GW98-177	22060	26.13	1854.49	3708.98	colon tumor	1.48
colon normal GW98-561	23514	26.82	1165.06	2330.12	colon normal	
colon tumor GW98-560	23513	25.75	2390.26	4780.52	colon tumor	2.05
colon normal GW98-894	24691	26.06	1948.57	3897.14	colon normal	
colon tumor GW98-893	24690	26.59	1362.55	2725.10	colon tumor	-1.43
lung normal GW98-3	20742	22.77	17753	35506.00	lung normal	
lung tumor GW98-2	20741	26.17	1803.8	3607.60	lung tumor	-9.84
lung normal GW97-179	20677	25.24	3370.88	6741.76	lung normal	
lung tumor GW97-178	20676	24.14	7057.92	14115.84	lung tumor	2.09
lung normal GW98-165	21922	23.87	8442.49	16884.98	lung normal	
lung tumor GW98-164	21921	24.08	7339.83	14679.66	lung tumor	-1.15
lung normal GW98-282	22584	25.51	2804.42	5608.84	lung normal	
lung tumor GW98-281	22583	24.2	6787.31	13574.62	lung tumor	2.42
breast normal GW00-392	28750	25.7	2480.5	2480.50	breast normal	
breast tumor GW00-391	28746	25.77	2364.2	4728.40	breast tumor	1.91
breast normal GW00-413	28798	26.06	1948.1	1948.10	breast normal	
breast tumor GW00-412	28797	27.21	894.11	1788.22	breast tumor	-1.09
breast normal GW00-235:238	27592-95	26.64	1317.83	1317.83	breast normal	
breast tumor GW00-231:234	27588-91	23.91	8225.11	8225.11	breast tumor	6.24
breast normal GW98-621	23656	24.46	5693.73	11387.46	breast normal	
breast tumor GW98-620	23655	23.91	8218.73	16437.46	breast tumor	1.44
brain normal BB99-542	25507	26.39	1553.13	3106.26	brain normal	
brain normal BB99-406	25509	26.63	1325.63	2651.26	brain normal	
brain normal BB99-904	25546	27.05	1001.6	2003.20	brain normal	
brain stage 5 ALZ BB99-874	25502	26.97	1052.15	2104.30	brain stage 5 ALZ	-1.23
brain stage 5 ALZ BB99-887	25503	25.28	3289.99	6579.98	brain stage 5 ALZ	2.54
brain stage 5 ALZ BB99-862	25504	26.24	1725.06	3450.12	brain stage 5 ALZ	1.33
brain stage 5 ALZ BB99-	25542	26.12	1864.26	3728.52	brain stage 5 ALZ	1.44

927						
CT lung KC	normal	24.74	4711.99	9423.98	CT lung	
lung 26 KC	normal	27.78	611.36	611.36	lung 26	
lung 27 KC	normal	28.27	439.19	439.19	lung 27	
lung 24 KC	COPD	26.92	1091.11	1091.11	lung 24	-2.56
lung 28 KC	COPD	26.93	1085.65	1085.65	lung 28	-2.57
lung 23 KC	COPD	27.19	909.68	909.68	lung 23	-3.07
lung 25 KC	normal	27.62	678.79	678.79	lung 25	
asthmatic lung ODO3112	29321	25.33	3173.52	3173.52	asthmatic lung	1.14
asthmatic lung ODO3433	29323	25.36	3106.89	6213.78	asthmatic lung	2.23
asthmatic lung ODO3397	29322	23.81	8809.42	17618.84	asthmatic lung	6.32
asthmatic lung ODO4928	29325	24.76	4649.98	9299.96	asthmatic lung	3.34
endo cells KC	control	26	2021.13	2021.13	endo cells	
endo VEGF KC		25.78	2343.21	2343.21	endo VEGF	1.16
endo bFGF KC		26.7	1264.03	1264.03	endo bFGF	-1.60
heart Clontech	normal	26.62	1330.64	2661.28	heart	
heart (T-1) ischemic	29417	27.07	984.33	1968.66	heart T-1	-1.35
heart (T-14) non-obstructive DCM	29422	26.11	1877.75	3755.50	heart T-14	1.41
heart (T-3399) DCM	29426	26.34	1608.79	3217.58	heart T-3399	1.21
adenoid GW99-269	26162	27.64	670.25	1340.50	adenoid	
tonsil GW98-280	22582	27.61	684.15	1368.30	tonsil	
T cells PC00314	28453	25.95	2098.64	4197.28	T cells	
PBMNC		31.16	63.19	63.19	PBMNC	
monocyte		31.32	56.63	113.26	monocyte	
B cells PC00665	28455	26.34	1609.52	3219.04	B cells	
dendritic cells 28441		28.25	444.68	889.36	dendritic cells	
neutrophils	28440	26.11	1874.13	1874.13	neutrophils	
eosinophils	28446	26.39	1553.82	3107.64	eosinophils	
BM unstim		31.45	51.76	51.76	BM unstim	
BM stim		31.28	58.37	58.37	BM stim	1.13
osteo dif		24.62	5118.74	5118.74	osteo dif	1.70
osteo undif		25.41	3015.6	3015.60	osteo undif	
chondrocytes		22.12	27351.89	68379.73	chondrocytes	
OA Synovium IP12/01	29462	24.5	5551.61	5551.61	OA Synovium	
OA Synovium NP10/01	29461	25.1	3711.29	7422.58	OA Synovium	
OA Synovium NP57/00	28464	24.5	5537.1	11074.20	OA Synovium	
RA Synovium NP03/01	28466	26.45	1492.95	2985.90	RA Synovium	
RA Synovium NP71/00	28467	24.44	5783.96	11567.92	RA Synovium	
RA Synovium NP45/00	28475	25.94	2112.54	4225.08	RA Synovium	
OA bone (biobank)	29217	26.16	1811.72	1811.72	OA bone (biobank)	
OA bone Sample 1	J. Emory	24.54	5399.31	10798.62	OA bone	
OA bone Sample 2	J. Emory	26.07	1931.94	3863.88	OA bone	
Cartilage (pool)	Normal	25.09	3730.42	7460.84	Cartilage (pool)	
Cartilage (pool)	OA	25.79	2328.66	4657.32	Cartilage (pool)	-1.60
PBL uninfected	28441	26.95	1068.16	2136.32	PBL uninfected	
PBL HIV IIIB	28442	28.41	401.86	803.72	PBL HIV IIIB	-2.66

MRC5 uninfected (100%)	29158	22.28	24694.87	49389.74	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	29.07	256.64	513.28	MRC5 HSV strain F	-96.22
W12 cells	29179	28.37	410.68	821.36	W12 cells	
Keratinocytes	29180	29.12	249.25	498.50	Keratinocytes	
B-actin control		27.53	721.15			
genomic		26.92	1091.74			
1.00E+05		19.96	100000			
1.00E+05		20.19	100000			
1.00E+04		23.43	10000			
1.00E+04		23.34	10000			
1.00E+03		26.64	1000			
1.00E+03		26.8	1000			
1.00E+02		31.34	100			
1.00E+02		31.48	100			
1.00E+01		34.9	10			
1.00E+01		34.19	10			
1.00E-00		40	0			
1.00E-00		35.53	1			
NTC		40	0			

Gene Name sbg1151bSREC

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	3.69
colon tumor	1.48
colon tumor	2.05
colon tumor	-1.43
lung tumor	-9.84
lung tumor	2.09
lung tumor	-1.15
lung tumor	2.42
breast tumor	1.91
breast tumor	-1.09
breast tumor	6.24
breast tumor	1.44
brain stage 5 ALZ	-1.23
brain stage 5 ALZ	2.54
brain stage 5 ALZ	1.33
brain stage 5 ALZ	1.44
lung 24	-2.56
lung 28	-2.57
lung 23	-3.07
asthmatic lung	1.14
asthmatic lung	2.23
asthmatic lung	6.32
asthmatic lung	3.34
endo VEGF	1.16
endo bFGF	-1.60
heart T-1	-1.35

heart T-14	1.41
heart T-3399	1.21
BM stim	1.13
osteo dif	1.70
Cartilage (pool)	-1.60
PBL HIV IIIB	-2.66
MRC5 HSV strain F	-96.22

Gene Name sbg1399854ANK

Low overall expression. Highest normal expression is seen in the whole brain, fetal brain, and liver.

5

Good levels of expression are seen in all of the samples representing the female reproductive system. Highest disease expression is seen in the normal and Alzheimer's brain samples as well as in the dendritic cells. Upregulation in 2 of 4 colon tumor samples and in 2 of 4 breast tumor samples as well as downregulation in 2 of 4 lung tumor samples implicates this gene in cancers of the colon, breast, and lung. Downregulation in 3 of 3 COPD samples and in 2 of 4 asthmatic lung samples suggests a potential role for this gene in chronic obstructive pulmonary disorder and asthma. Downregulation in the OA cartilage sample as well as corroborating low expression in the normal chondrocytes and many of the immune cells suggests involvement in osteoarthritis.

10

Upregulation in the HSV-infected MRC5 cells suggests that this gene may be a host factor in HSV.

Sample sbg1399854ANK	Ct (sample 1 and 2)	Mean GOI copies (sample 1)	Mean GOI copies (sample 2)	Average GOI Copies	18S rRNA (ng)	50 ng/18S rRNA (ng)	copies of mRNA detecte d/50 ng total RNA
Subcutaneous Adipocytes Zenbio	40, 40	0	0	0.00	3.06	16.34	0.00
Subcutaneous Adipose Zenbio	40, 40	1.83	1.77	1.80	0.96	52.36	94.24
Adrenal Gland Clontech	40, 40	1.75	0	0.88	0.61	81.97	71.72
Whole Brain Clontech	28.57, 28.35	944.29	1058.09	1001.19	7.24	6.91	6914.30
Fetal Brain Clontech	36.57, 34.65	14.38	39.28	26.83	0.48	103.95	2788.98
Cerebellum Clontech	37.21, 36.71	10.3	13.37	11.84	2.17	23.04	272.70
Cervix	36.3, 40	16.52	0	8.26	2.42	20.66	170.66
Colon	36.17, 35.71	17.73	22.5	20.12	2.71	18.45	371.13
Endometrium	40, 36.1	0	18.41	9.21	0.73	68.21	627.90
Esophagus	40, 40	0	1.58	0.79	1.37	36.50	28.83
Heart Clontech	40, 40	0	0	0.00	1.32	37.88	0.00
Hypothalamus	40, 40	0	0	0.00	0.32	155.28	0.00
Ileum	40, 40	0	0	0.00	2.58	19.38	0.00
Jejunum	34.07, 34.37	53.18	45.33	49.26	6.60	7.58	373.14
Kidney	37.55, 40	8.58	0	4.29	2.12	23.58	101.18
Liver	36.53, 35.62	14.69	23.59	19.14	1.50	33.33	638.00
Fetal Liver Clontech	34.56, 34.61	41.04	40.04	40.54	10.40	4.81	194.90
Lung	40, 40	0	0	0.00	2.57	19.46	0.00
Mammary Gland Clontech	39.07, 39.45	3.89	3.18	3.54	13.00	3.85	13.60
Myometrium	39.5, 35.37	3.1	26.93	15.02	2.34	21.37	320.83
Omentum	40, 36.18	0	17.61	8.81	3.94	12.69	111.74
Ovary	35.87, 34.34	20.75	46.22	33.49	4.34	11.52	385.77

Pancreas	40, 40	0	0	0.00	0.81	61.80	0.00
Head of Pancreas	40, 39.79	0	2.66	1.33	1.57	31.85	42.36
Parotid Gland	35.2, 38.6	29.46	4.97	17.22	5.48	9.12	157.07
Placenta Clontech	40, 38.14	0	6.32	3.16	5.26	9.51	30.04
Prostate	40, 40	0	0	0.00	3.00	16.67	0.00
Rectum	40, 39.2	0	3.63	1.82	1.23	40.65	73.78
Salivary Gland Clontech	40, 39.19	2.19	3.64	2.92	7.31	6.84	19.94
Skeletal Muscle Clontech	40, 39.37	0	3.32	1.66	1.26	39.68	65.87
Skin	40, 40	0	2.09	1.05	1.21	41.32	43.18
Small Intestine Clontech	40, 40	1.44	0	0.72	0.98	51.07	36.77
Spleen	35.36, 40	27.05	1.84	14.45	4.92	10.16	146.80
Stomach	40, 37.03	1.93	11.29	6.61	2.73	18.32	121.06
Testis Clontech	40, 37.99	0	6.82	3.41	0.57	87.87	299.65
Thymus Clontech	38.47, 35.55	5.32	24.52	14.92	9.89	5.06	75.43
Thyroid	40, 40	0	2.15	1.08	2.77	18.05	19.40
Trachea Clontech	35.37, 36.67	26.97	13.66	20.32	9.71	5.15	104.61
Urinary Bladder	39.07, 40	3.89	1.42	2.66	5.47	9.14	24.27
Uterus	36.01, 33.41	19.29	75.06	47.18	5.34	9.36	441.71
genomic	29.57	558.84					
b-actin	27.57	1592.66					
1.00E+05	19.91	100000					
1.00E+05	20.08	100000					
1.00E+04	23.79	10000					
1.00E+04	24.06	10000					
1.00E+03	27.72	1000					
1.00E+03	28.29	1000					
1.00E+02	31.95	100					
1.00E+02	33.62	100					
1.00E+01	39.75	10					
1.00E+01	35.41	10					
1.00E-00	40	0					
1.00E-00	40	0					
NTC	40	-1					
NTC	40	-1					

Sample sbg1399854ANK	Reg number (GSK identifier)	Ct	Mean GOI copies	copies of mRNA detecte d/50 ng total RNA	Sample	Fold Change in Disease Populati on
colon normal GW98-167	21941	35.32	22.34	44.68	colon normal	
colon tumor GW98-166	21940	34.14	47.5	95.00	colon tumor	2.13
colon normal GW98-178	22080	36.16	13.07	26.14	colon normal	
colon tumor GW98-177	22060	35.58	18.93	37.86	colon tumor	1.45

colon normal GW98-561	23514	36.58	10.03	20.06	colon normal	
colon tumor GW98-560	23513	32.61	126.48	252.96	colon tumor	12.61
colon normal GW98-894	24691	35.61	18.62	37.24	colon normal	
colon tumor GW98-893	24690	33.24	84.75	169.50	colon tumor	4.55
lung normal GW98-3	20742	34.77	31.8	63.60	lung normal	
lung tumor GW98-2	20741	33.63	66.03	132.06	lung tumor	2.08
lung normal GW97-179	20677	34.76	32.04	64.08	lung normal	
lung tumor GW97-178	20676	34.44	39.23	78.46	lung tumor	1.22
lung normal GW98-165	21922	35.18	24.44	48.88	lung normal	
lung tumor GW98-164	21921	37.99	4.06	8.12	lung tumor	-6.02
lung normal GW98-282	22584	33.64	65.37	130.74	lung normal	
lung tumor GW98-281	22583	37.3	6.34	12.68	lung tumor	-10.31
breast normal GW00-392	28750	36.29	12.08	12.08	breast normal	
breast tumor GW00-391	28746	36.14	13.29	26.58	breast tumor	2.20
breast normal GW00-413	28798	37.08	7.29	7.29	breast normal	
breast tumor GW00-412	28797	33.26	83.58	167.16	breast tumor	22.93
breast normal GW00-235:238	27592-95	38.93	2.24	2.24	breast normal	
breast tumor GW00-231:234	27588-91	36.57	10.08	10.08	breast tumor	4.50
breast normal GW98-621	23656	34.9	29.32	58.64	breast normal	
breast tumor GW98-620	23655	36.11	13.51	27.02	breast tumor	-2.17
brain normal BB99-542	25507	29.6	866.9	1733.80	brain normal	
brain normal BB99-406	25509	31.93	194.87	389.74	brain normal	
brain normal BB99-904	25546	30.38	526.58	1053.16	brain normal	
brain stage 5 ALZ BB99-874	25502	32.7	119.57	239.14	brain stage 5 ALZ	-4.43
brain stage 5 ALZ BB99-887	25503	30.08	634.97	1269.94	brain stage 5 ALZ	1.20
brain stage 5 ALZ BB99-862	25504	29.7	809.22	1618.44	brain stage 5 ALZ	1.53
brain stage 5 ALZ BB99-927	25542	29.93	700.82	1401.64	brain stage 5 ALZ	1.32
CT lung	normal	35.1	25.82	51.64	CT lung Nml	
lung 26	normal	36.74	9.07		lung 26 Nml	
lung 27	normal	40	0	0.00	lung 27 Nml	
lung 24	COPD	40	2.5	2.50	lung 24 COPD	-7.11
lung 28	COPD	40	0	0.00	lung 28 COPD	-17.77
lung 23	COPD	40	0	0.00	lung 23 COPD	-17.77
lung 25	normal	39.39	1.67	1.67	lung 25 Nml	
asthmatic lung ODO3112	29321	40	0	0.00	asthmatic lung	-17.77
asthmatic lung ODO3433	29323	37	7.68	15.36	asthmatic lung	-1.16
asthmatic lung ODO3397	29322	36.08	13.8	27.60	asthmatic lung	1.55
asthmatic lung ODO4928	29325	40	0	0.00	asthmatic lung	-17.77
endo cells	control	40	0	0.00	endo cells	
endo VEGF		40	0	0.00	endo VEGF	0.00
endo bFGF		35.68	17.77	17.77	endo bFGF	17.77
heart Clontech	normal	35.03	26.95	53.90	heart	
heart (T-1) ischemic	29417	36.36	11.53	23.06	heart (T-1) ischemic	-2.34

heart (T-14) non-obstructive DCM	29422	34.57	36.11	72.22	heart (T-14) non-obstructive DCM	1.34
heart (T-3399) DCM	29426	36.25	12.37	24.74	heart (T-3399) DCM	-2.18
adenoid GW99-269	26162	38.51	2.92	5.84	adenoid	
tonsil GW98-280	22582	35.05	26.54	53.08	tonsil	
T cells PC00314	28453	35.5	19.98	39.96	T cells	
PBMNC		40	0	0.00	PBMNC	
monocyte		40	0	0.00	monocyte	
B cells PC00665	28455	33.78	59.82	119.64	B cells	
dendritic cells	28441	29.33	1026.14	2052.28	dendritic cells	
neutrophils	28440	31.3	292.56	292.56	neutrophils	
eosinophils	28446	35.97	14.79	29.58	eosinophils	
BM unstim		35.56	19.16	19.16	BM unstim	
BM stim	treated	34.79	31.48	31.48	BM stim	1.64
osteo dif	treated	40	2.59	2.59	osteo dif	2.59
osteo undif		40	0	0.00	osteo undif	
chondrocytes		37.11	7.15	17.88	chondrocytes	
OA Synovium IP12/01	29462	35.95	14.93	14.93	OA Synovium	
OA Synovium NP10/01	29461	35.74	17.17	34.34	OA Synovium	
OA Synovium NP57/00	28464	39.09	2.02	4.04	OA Synovium	
RA Synovium NP03/01	28466	38.03	3.97	7.94	RA Synovium	
RA Synovium NP71/00	28467	35.08	26.03	52.06	RA Synovium	
RA Synovium NP45/00	28475	37.11	7.13	14.26	RA Synovium	
OA bone (biobank)	29217	33.76	60.54	60.54	OA bone (biobank)	
OA bone Sample 1	J. Emory	33.35	78.68	157.36	OA bone	
OA bone Sample 2	J. Emory	34.15	47.2	94.40	OA bone	
Cartilage (pool)	Normal	35.05	26.63	53.26	Nml Cartilage (pool)	
Cartilage (pool)	OA	37.42	5.87	11.74	OA Cartilage (pool)	-4.54
PBL uninfected	28441	33.95	53.63	107.26	PBL uninfected	
PBL HIV IIIB	28442	33.3	81.2	162.40	PBL HIV IIIB	1.51
MRC5 uninfected (100%)	29158	39.41	1.64	3.28	MRC5 uninfected (100%)	
MRC5 HSV strain F	29178	35.73	17.22	34.44	MRC5 HSV strain F	10.50
W12 cells	29179	35.08	26.08	52.16	W12 cells	
Keratinocytes	29180	36.69	9.33	18.66	Keratinocytes	
B-actin control		28.13	2213.67			
genomic		29.03	1240.79			
1.00E+05		22.03	100000			
1.00E+05		22.36	100000			
1.00E+04		25.68	10000			
1.00E+04		25.78	10000			
1.00E+03		29.01	1000			
1.00E+03		28.67	1000			
1.00E+02		33.46	100			
1.00E+02		40	100			

1.00E+01		38.75	10			
1.00E+01		40	10			
1.00E-00		40	0			
1.00E-00		38.6	1			
NTC		40	0			
*lung 26 Normal has been omitted due to multiple amplification failures from that sample						

Gene Name sbg1399854ANK

Disease tissues	Fold Change in Disease Population Relative to Normal
colon tumor	2.13
colon tumor	1.45
colon tumor	12.61
colon tumor	4.55
lung tumor	2.08
lung tumor	1.22
lung tumor	-6.02
lung tumor	-10.31
breast tumor	2.20
breast tumor	22.93
breast tumor	4.50
breast tumor	-2.17
brain stage 5 ALZ	-4.43
brain stage 5 ALZ	1.20
brain stage 5 ALZ	1.53
brain stage 5 ALZ	1.32
lung 24	-7.11
lung 28	-17.77
lung 23	-17.77
asthmatic lung	-17.77
asthmatic lung	-1.16
asthmatic lung	1.55
asthmatic lung	-17.77
endo VEGF	0.00
endo bFGF	17.77
heart T-1	-2.34
heart T-14	1.34
heart T-3399	-2.18
BM stim	1.64
osteo dif	2.59
Cartilage (pool)	-4.54
PBL HIV IIIB	1.51
MRC5 HSV strain F	10.50

Table V. Additional diseases based on mRNA expression in specific tissues

Tissue Expression	Additional Diseases
Brain	Neurological and psychiatric diseases, including Alzheimers, parasupranuclear palsey, Huntington's disease, myotonic dystrophy, anorexia, depression, schizophrenia, headache, amnesias, anxiety disorders, sleep disorders, multiple sclerosis
Heart	Cardiovascular diseases, including congestive heart failure, dilated cardiomyopathy, cardiac arrhythmias, Hodgson's Disease, myocardial infarction, cardiac arrhythmias
Lung	Respiratory diseases, including asthma, Chronic Obstructive Pulmonary Disease, cystic fibrosis, acute bronchitis, adult respiratory distress syndrome
Liver	Dyslipidemia, hypercholesterolemia, hypertriglyceridemia, cirrhosis, hepatic encephalopathy, fatty hepatocirrhosis, viral and nonviral hepatitis, Type II Diabetes Mellitis, impaired glucose tolerance
Kidney	Renal diseases, including acute and chronic renal failure, acute tubular necrosis, cystinuria, Fanconi's Syndrome, glomerulonephritis, renal cell carcinoma, renovascular hypertension
Skeletal muscle	Eulenburg's Disease, hypoglycemia, obesity, tendinitis, periodic paralyses, malignant hyperthermia, paramyotonia congenita, myotonia congenita
Intestine	Gastrointestinal diseases, including Myotonia congenita, Ileus, Intestinal Obstruction, Tropical Sprue, Pseudomembranous Enterocolitis
Spleen/lymph	Lymphangiectasia, hypersplenism, angiomas, ankylosing spondylitis, Hodgkin's Disease, macroglobulinemia, malignant lymphomas, rheumatoid arthritis
Placenta	Choriocarcinoma, hydatidiform mole, placenta previa
Testis	Testicular cancer, male reproductive diseases, including low testosterone and male infertility
Pancreas	Diabetic ketoacidosis, Type 1 & 2 diabetes, obesity, impaired glucose tolerance

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
 - 5 (a) an isolated polypeptide encoded by a polynucleotide comprising a sequence set forth in Table I;
 - (b) an isolated polypeptide comprising a polypeptide sequence set forth in Table I; and
 - (c) a polypeptide sequence of a gene set forth in Table I.
- 10 2. An isolated polynucleotide selected from the group consisting of:
 - (a) an isolated polynucleotide comprising a polynucleotide sequence set forth in Table I;
 - (b) an isolated polynucleotide of a gene set forth in Table I;
 - (c) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide set forth in Table I;
 - 15 (d) an isolated polynucleotide encoding a polypeptide set forth in Table I;
 - (e) a polynucleotide which is an RNA equivalent of the polynucleotide of (a) to (d); or a polynucleotide sequence complementary to said isolated polynucleotide.
- 20 3. An expression vector comprising a polynucleotide capable of producing a polypeptide of claim 1 when said expression vector is present in a compatible host cell.
4. A process for producing a recombinant host cell which comprises the step of introducing an expression vector comprising a polynucleotide capable of producing a polypeptide of claim 1 into a cell such that the host cell, under appropriate culture conditions, produces said
25 polypeptide.
5. A recombinant host cell produced by the process of claim 4.
6. A membrane of a recombinant host cell of claim 5 expressing said polypeptide.
- 30 7. A process for producing a polypeptide which comprises culturing a host cell of claim 5 under conditions sufficient for the production of said polypeptide and recovering said polypeptide from the culture.

SEQUENCE LISTING

<110> SMITHKLINE BEECHAM CORPORATION
 SMITHKLINE BEECHAM p.l.c.
 GLAXO GROUP, LIMITED

<120> NOVEL COMPOUNDS

<130> GP50034

<140> TO BE ASSIGNED

<141> 2001-09-13

<150> 60/232,463

<151> 2000-09-13

<150> 60/232,455

<151> 2000-09-13

<150> 60/237,293

<151> 2000-10-02

<150> 60/246,269

<151> 2000-11-07

<150> 60/252,049

<151> 2000-11-20

<160> 88

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1707

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<211> 984

<212> DNA

<213> Homo sapiens

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<211> 1296

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<211> 1116

<212> DNA

<213> Homo sapiens

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<211> 759

<212> DNA

<213> Homo sapiens

<400> 23

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<211> 1494

<212> DNA

<213> Homo sapiens

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<211> 1315

<212> DNA

<213> Homo sapiens

<400> 25

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<211> 927

<212> DNA

<213> Homo sapiens

<400> 26

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<210> 27

<211> 1344

<212> DNA

<213> Homo sapiens

<400> 27

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<210> 28

<211> 1375

<212> DNA

<213> Homo sapiens

<400> 28

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<210> 29

<211> 510

<212> DNA

<213> Homo sapiens

<400> 29

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<210> 30

<211> 561

<212> DNA

<213> Homo sapiens

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<210> 31

<211> 2028

<212> DNA

<213> Homo sapiens

<400> 31

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<210> 32

<211> 1458

<212> DNA

<213> Homo sapiens

<400> 32

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<210> 41

<211> 2494

<212> DNA

<213> Homo sapiens

<400> 41

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cgatcgctac	tgccagtgtc	tccgcggccg	ctgccaccct	gtggacggca	cgtgtgcctg	660
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cccccggaag	aagaccccc	tccagaagcc	gccgcgcaag	aagagccggg	aggcggcggg	2460
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<210> 42

<211> 2614

<212> DNA

<213> Homo sapiens

<400> 42

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cgtggcgccct	caggaactga	accctcgccg	ccgcaactg	tgccgtgctc	ccggctccca	180
ggtgcccacg	tgctgcgctg	gctggaggca	gcaaggggac	gagtgtggga	ttgcggtgtg	240
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ccgccacggc	tacttcgggtg	ccaactgcga	caccaagtgc	ccgcgccagt	tctggggccc	360
cgactgcaag	gagctgtgta	gctgccaccc	acacgggcag	tgcgaggacg	tgacaggcca	420
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cggcacgtgc	cacccccgga	gcggcgcggtg	ccgctgtgag	tccggctggt	ggggcgcgca	540
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cccccggaag	aagacccccca	tccagaagcc	gccgcgcaag	aagagccggg	aggcggcggg	2580
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<210> 43

<211> 402

<212> DNA

<213> Homo sapiens

<400> 43

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cgagacgagc	gcggccgcac	cgcactcagc	ctggcgctgg	agcgaggcca	cctggacgcc	180
gtgcagctgc	tggtgcagtt	cagccgtgac	cccagggcgg	ccgactctgc	gggcaacagc	240
ccgggtgatgt	gggcggcgcc	ctgcggccac	ggggcggtgc	tcgagttcct	gggtgcggctc	300
ttccgcgcgc	taggcctcgc	cctcgaccgc	accaaccgtg	cggggctcac	cgcgctgcaa	360
ctggccgcgc	cccgcggcca	cgggacctgt	gtgcaggccc	tc		402

<210> 44

<211> 975

<212> DNA

<213> Homo sapiens

<400> 44

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gactgccgcg	cggagcaggg	ccgtacgcgc	ctcatgggtg	ccgtggggct	gccggacccc	180
gcgctgcgcg	cgcgcttcgt	cgggctgctg	ctcgagcagg	gtgctgcagt	gaacctgcga	240
gacgagcgcg	gccgcaccgc	actcagcctg	gcgtgcgagc	gaggccacct	ggacgcccgtg	300
cagctgctgg	tgcagttcag	cggtgacccc	gaggcgcccg	actctgcggg	caacagcccc	360
gtgatgtggg	cggcgccctg	cggccacggg	gcggtgctcg	agttcctggg	gcggtccttc	420
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gccgcgcgcc	gcggccacgg	gacctcggcg	ggcggccacg	gcggcgaggc	tggtctcagcg	540
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atgagcctgg	ctctaggtgc	ggtaaccgag	gaggaggctg	cccgcctgcg	ggctggggcc	660
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gtgctggagg	gagcgccccc	aaccttagcg	caagccccc	ttggcctcag	ttcccacccg	780
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cccagcctgg	tcggggaggc	gccaggcccc	gagagtggcc	cggagttaga	ggccaacgct	900
ctgtctgtct	cgggtgcctg	gccgaaccct	tggcaggcgg	gcaccgaggc	tgtggtgctg	960
cgtgctcagc	ggtaa					975

<210> 45
 <211> 568
 <212> PRT
 <213> homo sapiens

<400> 45

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Met Lys Glu Ala Glu Met Asp Gly Glu Ala Val Arg Phe Cys Thr Asp
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          20          25          30
Ala Pro Ala Ala Pro Lys Ile Pro Arg Leu Val Gln Ala Thr Pro Ala
          35          40          45
Phe Met Ala Val Thr Leu Val Phe Ser Leu Val Thr Leu Phe Val Val
          50          55          60
Gly Lys Pro Pro Val Gln Gln Gln Thr Arg Pro Val Pro Lys Pro Val
65          70          75          80
Gln Ala Val Ile Leu Gly Asp Asn Ile Thr Gly His Leu Pro Phe Glu
          85          90          95
Pro Asn Asn His His His Phe Gly Arg Glu Ala Glu Met Arg Glu Leu
          100          105          110
Ile Gln Thr Phe Lys Gly His Met Glu Asn Ser Ser Ala Trp Val Val
          115          120          125
Glu Ile Gln Met Leu Lys Cys Arg Val Asp Asn Val Asn Ser Gln Leu
          130          135          140
Gln Val Leu Gly Asp His Leu Gly Asn Thr Asn Ala Asp Ile Gln Met
145          150          155          160
Val Lys Gly Val Leu Lys Asp Ala Thr Thr Leu Ser Leu Gln Thr Gln
          165          170          175
Met Leu Arg Ser Ser Leu Glu Gly Thr Asn Ala Glu Ile Gln Arg Leu
          180          185          190
Lys Glu Asp Leu Glu Lys Ala Asp Ala Leu Thr Phe Gln Thr Leu Asn
          195          200          205
Phe Leu Lys Ser Ser Leu Glu Asn Thr Ser Ile Glu Leu His Val Leu
          210          215          220
Ser Arg Gly Leu Glu Asn Ala Asn Ser Glu Ile Gln Met Leu Asn Ala
225          230          235          240
Arg Ala Asn Ala Glu Ile Gln Gly Leu Lys Glu Asn Leu Gln Asn Thr
          245          250          255
Asn Ala Leu Asn Ser Gln Thr Gln Ala Phe Ile Lys Ser Ser Phe Asp
          260          265          270
Asn Thr Ser Ala Glu Ile Gln Phe Leu Arg Gly His Leu Glu Arg Ala
          275          280          285
Gly Asp Glu Ile His Val Leu Lys Arg Asp Leu Lys Met Val Thr Ala
          290          295          300
Gln Thr Gln Lys Ala Asn Gly Arg Leu Asp Gln Thr Asp Thr Gln Ile
305          310          315          320
Gln Val Phe Lys Ser Glu Met Glu Asn Val Asn Thr Leu Asn Ala Gln
          325          330          335
Ile Gln Val Leu Asn Gly His Met Lys Asn Ala Ser Arg Glu Ile Gln
          340          345          350
Thr Leu Lys Gln Gly Met Lys Asn Ala Ser Ala Leu Thr Ser Gln Thr
          355          360          365
Gln Met Leu Asp Ser Asn Leu Gln Lys Ala Ser Ala Glu Ile Gln Arg
          370          375          380
Leu Arg Gly Asp Leu Glu Asn Thr Lys Ala Leu Thr Met Glu Ile Gln
385          390          395          400
Gln Glu Gln Ser Arg Leu Lys Thr Leu His Val Val Ile Thr Ser Gln
          405          410          415

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Glu Gln Leu Gln Arg Thr Gln Ser Gln Leu Leu Gln Met Val Leu Gln
 420 425 430
 Gly Trp Lys Phe Asn Gly Gly Ser Leu Tyr Tyr Phe Ser Ser Val Lys
 435 440 445
 Lys Ser Trp His Glu Ala Glu Gln Phe Cys Val Ser Gln Gly Ala His
 450 455 460
 Leu Ala Ser Val Ala Ser Lys Glu Glu Gln Ala Phe Leu Val Glu Phe
 465 470 475 480
 Thr Ser Lys Val Tyr Tyr Trp Ile Gly Leu Thr Asp Arg Gly Thr Glu
 485 490 495
 Gly Ser Trp Arg Trp Thr Asp Gly Thr Pro Phe Asn Ala Ala Gln Asn
 500 505 510
 Lys Ala Pro Val Val Phe Gly Phe Trp Glu Lys Asn Gln Ser Asp Asn
 515 520 525
 Trp Arg His Lys Asn Gly Gln Thr Glu Asp Cys Val Gln Ile Gln Gln
 530 535 540
 Lys Trp Asn Asp Met Thr Cys Asp Thr Pro Tyr Gln Trp Val Cys Lys
 545 550 555 560
 Lys Pro Met Gly Gln Gly Val Ala
 565

<210> 46

<211> 364

<212> PRT

<213> homo sapiens

<400> 46

Met Ser Arg Gln Gly Lys Leu Phe Ser Ala Phe Gly Val Gly Cys Cys
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 Val Thr Ala Gly Leu Pro Lys Asp Asp Asn Thr Pro Ser Thr Ile Ala
 20 25 30
 Asp Val His Asn Gly Tyr Thr Met Asn Val Val Glu Gln Val Leu Lys
 35 40 45
 Asp Ser Phe Val Leu Phe Phe Pro Gly Thr Leu Cys Asp Phe Pro Lys
 50 55 60
 Ile His His Gly Phe Leu Tyr Asp Glu Glu Asp Tyr Asn Pro Phe Ser
 65 70 75 80
 Gln Val Pro Thr Gly Glu Val Phe Tyr Tyr Ser Cys Glu Tyr Asn Phe
 85 90 95
 Val Ser Pro Ser Lys Ser Phe Trp Thr Arg Ile Thr Cys Thr Glu Glu
 100 105 110
 Gly Trp Ser Pro Thr Pro Lys Cys Leu Arg Met Cys Ser Phe Pro Phe
 115 120 125
 Val Lys Asn Gly His Ser Glu Ser Ser Gly Leu Ile His Leu Glu Gly
 130 135 140
 Asp Thr Val Gln Ile Ile Cys Asn Thr Gly Tyr Ser Leu Gln Asn Asn
 145 150 155 160
 Glu Lys Asn Ile Ser Cys Val Glu Arg Gly Trp Ser Thr Pro Pro Ile
 165 170 175
 Cys Ser Phe Thr Met Lys Thr Cys Gly Tyr Ile Pro Glu Leu Glu Tyr
 180 185 190
 Gly Tyr Val Gln Pro Ser Val Pro Pro Tyr Gln His Gly Val Ser Val
 195 200 205
 Glu Val Asn Cys Arg Asn Glu Tyr Ala Met Ile Gly Asn Asn Met Ile
 210 215 220
 Thr Cys Ile Asn Gly Ile Trp Thr Glu Leu Pro Met Cys Val Glu Ser
 225 230 235 240
 Thr Ala Tyr Cys Gly Pro Pro Pro Ser Ile Asn Asn Gly Asp Thr Thr

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                245                250                255
Ser Phe Pro Leu Ser Val Tyr Pro Pro Gly Ser Thr Val Thr Tyr Arg
                260                265                270
Cys Gln Ser Phe Tyr Lys Leu Gln Gly Ser Val Thr Val Thr Cys Arg
                275                280                285
Asn Lys Gln Trp Ser Glu Pro Pro Arg Cys Leu Asp Pro Cys Val Val
                290                295                300
Ser Glu Glu Asn Met Asn Lys Asn Asn Ile Gln Leu Lys Trp Arg Asn
305                310                315                320
Asp Gly Lys Leu Tyr Ala Lys Thr Gly Asp Ala Val Glu Phe Gln Cys
                325                330                335
Lys Phe Pro His Lys Ala Met Ile Ser Ser Pro Pro Phe Arg Ala Ile
                340                345                350
Cys Gln Glu Gly Lys Phe Glu Tyr Pro Ile Cys Glu
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<210> 47

<211> 327

<212> PRT

<213> homo sapiens

<400> 47

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Met Leu Leu Leu Phe Ser Val Ile Leu Ile Ser Trp Val Ser Thr Val
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                20                25                30
Leu Tyr Asp Glu Glu Asp Tyr Asn Pro Phe Ser Gln Val Pro Thr Gly
35                40                45
Glu Val Phe Tyr Tyr Ser Cys Glu Tyr Asn Phe Val Ser Pro Ser Lys
50                55                60
Ser Phe Trp Thr Arg Ile Thr Cys Thr Glu Glu Gly Trp Ser Pro Thr
65                70                75                80
Pro Lys Cys Leu Arg Met Cys Ser Phe Pro Phe Val Lys Asn Gly His
                85                90                95
Ser Glu Ser Ser Gly Leu Ile His Leu Glu Gly Asp Thr Val Gln Ile
                100                105                110
Ile Cys Asn Thr Gly Tyr Ser Leu Gln Asn Asn Glu Lys Asn Ile Ser
                115                120                125
Cys Val Glu Arg Gly Trp Ser Thr Pro Pro Ile Cys Ser Phe Thr Met
130                135                140
Lys Thr Cys Gly Tyr Ile Pro Glu Leu Glu Tyr Gly Tyr Val Gln Pro
145                150                155                160
Ser Val Pro Pro Tyr Gln His Gly Val Ser Val Glu Val Asn Cys Arg
                165                170                175
Asn Glu Tyr Ala Met Ile Gly Asn Asn Met Ile Thr Cys Ile Asn Gly
180                185                190
Ile Trp Thr Glu Leu Pro Met Cys Val Glu Ser Thr Ala Tyr Cys Gly
195                200                205
Pro Pro Pro Ser Ile Asn Asn Gly Asp Thr Thr Ser Phe Pro Leu Ser
210                215                220
Val Tyr Pro Pro Gly Ser Thr Val Thr Tyr Arg Cys Gln Ser Phe Tyr
225                230                235                240
Lys Leu Gln Gly Ser Val Thr Val Thr Cys Arg Asn Lys Gln Trp Ser
                245                250                255
Glu Pro Pro Arg Cys Leu Asp Pro Cys Val Val Ser Glu Glu Asn Met
260                265                270
Asn Lys Asn Asn Ile Gln Leu Lys Trp Arg Asn Asp Gly Lys Leu Tyr
275                280                285

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Ala Lys Thr Gly Asp Ala Val Glu Phe Gln Cys Lys Phe Pro His Lys
 290 295 300
 Ala Met Ile Ser Ser Pro Phe Arg Ala Ile Cys Gln Glu Gly Lys
 305 310 315 320
 Phe Glu Tyr Pro Ile Cys Glu
 325

<210> 48
 <211> 154
 <212> PRT
 <213> homo sapiens

<400> 48
 Met Ala Pro Ala Arg Ala Gly Cys Cys Pro Leu Leu Leu Leu Leu Leu
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 Gly Leu Trp Val Ala Glu Val Leu Val Arg Ala Lys Pro Lys Asp Met
 20 25 30
 Thr Ser Ser Gln Trp Phe Lys Thr Gln His Val Gln Pro Ser Pro Gln
 35 40 45
 Ala Cys Asn Ser Ala Met Ser Ile Ile Asn Lys Tyr Thr Glu Arg Cys
 50 55 60
 Lys Asp Leu Asn Thr Phe Leu His Glu Pro Phe Ser Ser Val Ala Ile
 65 70 75 80
 Thr Cys Gln Thr Pro Asn Ile Ala Cys Lys Asn Ser Cys Lys Asn Cys
 85 90 95
 His Gln Ser His Gly Pro Met Ser Leu Thr Met Gly Glu Leu Thr Ser
 100 105 110
 Gly Lys Tyr Pro Asn Cys Arg Tyr Lys Glu Lys His Leu Asn Thr Pro
 115 120 125
 Tyr Ile Val Ala Cys Asp Pro Pro Gln Gln Gly Asp Pro Gly Tyr Pro
 130 135 140
 Leu Val Pro Val His Leu Asp Lys Val Val
 145 150

<210> 49
 <211> 502
 <212> PRT
 <213> homo sapiens

<400> 49
 Met Arg Gln Leu Gly Gly Ser Leu Arg Pro Pro Arg Ala Ala His Gly
 1 5 10 15
 Ala Glu Pro Leu Pro Ser Ala Leu Gly Pro Cys Ala Gly Gly Asp Arg
 20 25 30
 Asp Leu Gly Arg Gly Thr Pro Gly Trp Glu Pro Arg Arg Ala Arg Val
 35 40 45
 Pro Ile His Glu Gln Val Asp Pro Pro Arg Glu Gly Pro His Leu Phe
 50 55 60
 Gln Asn Leu Leu Leu Phe Leu Trp Ala Leu Leu Asn Cys Gly Leu Gly
 65 70 75 80
 Val Ser Ala Gln Gly Pro Gly Glu Trp Thr Pro Trp Val Ser Trp Thr
 85 90 95
 Arg Cys Ser Ser Ser Cys Gly Arg Gly Val Ser Val Arg Ser Arg Arg
 100 105 110
 Cys Leu Arg Leu Pro Gly Glu Glu Pro Cys Trp Gly Asp Ser His Glu
 115 120 125
 Tyr Arg Leu Cys Gln Leu Pro Asp Cys Pro Pro Gly Ala Val Pro Phe

130	135	140
Arg Asp Leu Gln Cys Ala	Leu Tyr Asn Gly Arg	Pro Val Leu Gly Thr
145	150	155
Gln Lys Thr Tyr Gln Trp	Val Pro Phe His Gly	Ala Pro Asn Gln Cys
165	170	175
Asp Leu Asn Cys Leu Ala	Glu Gly His Ala Phe	Tyr His Ser Phe Gly
180	185	190
Arg Val Leu Asp Gly Thr	Ala Cys Ser Pro Gly	Ala Gln Gly Val Cys
195	200	205
Val Ala Gly Arg Cys Leu	Ser Ala Gly Cys Asp	Gly Leu Leu Gly Ser
210	215	220
Gly Ala Leu Glu Asp Arg	Cys Gly Arg Cys Gly	Gly Ala Asn Asp Ser
225	230	235
Cys Leu Phe Val Gln Arg	Val Phe Arg Asp Ala	Gly Ala Phe Ala Gly
245	250	255
Tyr Trp Asn Val Thr Leu	Ile Pro Glu Gly Ala	Arg His Ile Arg Val
260	265	270
Glu His Arg Ser Arg Asn	His Leu Gly Ile Leu	Gly Ser Leu Met Gly
275	280	285
Gly Asp Gly Arg Tyr Val	Leu Asn Gly His Trp	Val Val Ser Pro Pro
290	295	300
Gly Thr Tyr Glu Ala Ala	Gly Thr His Val Val	Tyr Thr Arg Asp Thr
305	310	315
Gly Pro Gln Glu Thr Leu	Gln Ala Ala Gly Pro	Thr Ser His Asp Leu
325	330	335
Leu Leu Gln Val Leu Leu	Gln Glu Pro Asn Pro	Gly Ile Glu Phe Glu
340	345	350
Phe Trp Leu Pro Arg Glu	Arg Tyr Ser Pro Phe	Gln Ala Arg Val Gln
355	360	365
Ala Leu Gly Trp Pro Leu	Arg Gln Pro Gln Pro	Arg Gly Val Glu Pro
370	375	380
Gln Pro Pro Ala Ala Pro	Ala Val Thr Pro Ala	Gln Thr Pro Thr Leu
385	390	395
Ala Pro Val Phe Gln Ala	Arg Val Leu Gly His	His His His Gln Ala
405	410	415
Glu Thr Arg Tyr Glu Val	Arg Ile Gln Leu Val	Tyr Lys Asn Arg Ser
420	425	430
Pro Leu Arg Ala Arg Glu	Tyr Val Trp Ala Pro	Gly His Cys Pro Cys
435	440	445
Pro Met Leu Ala Pro His	Arg Asp Tyr Leu Met	Ala Val Gln Arg Leu
450	455	460
Val Ser Pro Asp Gly Thr	Gln Asp Gln Leu Leu	Leu Pro His Ala Gly
465	470	475
Tyr Ala Arg Pro Trp Ser	Pro Ala Glu Asp Ser	Arg Ile Arg Leu Thr
485	490	495
Ala Arg Arg Cys Pro Gly		
500		

<210> 50

<211> 451

<212> PRT

<213> homo sapiens

<400> 50

Met Asp Ser Ala Pro Leu	Phe Pro Arg Pro His	Leu Phe Gln Asn Leu
1	5	10
Leu Leu Phe Leu Trp	Ala Leu Leu Asn Cys	Gly Leu Gly Val Ser
20	25	30

Gln Gly Pro Gly Glu Trp Thr Pro Trp Val Ser Trp Thr Arg Cys Ser
 35 40 45
 Ser Ser Cys Gly Arg Gly Val Ser Val Arg Ser Arg Arg Cys Leu Arg
 50 55 60
 Leu Pro Gly Glu Glu Pro Cys Trp Gly Asp Ser His Glu Tyr Arg Leu
 65 70 75 80
 Cys Gln Leu Pro Asp Cys Pro Pro Gly Ala Val Pro Phe Arg Asp Leu
 85 90 95
 Gln Cys Ala Leu Tyr Asn Gly Arg Pro Val Leu Gly Thr Gln Lys Thr
 100 105 110
 Tyr Gln Trp Val Pro Phe His Gly Ala Pro Asn Gln Cys Asp Leu Asn
 115 120 125
 Cys Leu Ala Glu Gly His Ala Phe Tyr His Ser Phe Gly Arg Val Leu
 130 135 140
 Asp Gly Thr Ala Cys Ser Pro Gly Ala Gln Gly Val Cys Val Ala Gly
 145 150 155 160
 Arg Cys Leu Ser Ala Gly Cys Asp Gly Leu Leu Gly Ser Gly Ala Leu
 165 170 175
 Glu Asp Arg Cys Gly Arg Cys Gly Gly Ala Asn Asp Ser Cys Leu Phe
 180 185 190
 Val Gln Arg Val Phe Arg Asp Ala Gly Ala Phe Ala Gly Tyr Trp Asn
 195 200 205
 Val Thr Leu Ile Pro Glu Gly Ala Arg His Ile Arg Val Glu His Arg
 210 215 220
 Ser Arg Asn His Leu Gly Ile Leu Gly Ser Leu Met Gly Gly Asp Gly
 225 230 235 240
 Arg Tyr Val Leu Asn Gly His Trp Val Val Ser Pro Pro Gly Thr Tyr
 245 250 255
 Glu Ala Ala Gly Thr His Val Val Tyr Thr Arg Asp Thr Gly Pro Gln
 260 265 270
 Glu Thr Leu Gln Ala Ala Gly Pro Thr Ser His Asp Leu Leu Gln
 275 280 285
 Val Leu Leu Gln Glu Pro Asn Pro Gly Ile Glu Phe Glu Phe Trp Leu
 290 295 300
 Pro Arg Glu Arg Tyr Ser Pro Phe Gln Ala Arg Val Gln Ala Leu Gly
 305 310 315 320
 Trp Pro Leu Arg Gln Pro Gln Pro Arg Gly Val Glu Pro Gln Pro Pro
 325 330 335
 Ala Ala Pro Ala Val Thr Pro Ala Gln Thr Pro Thr Leu Ala Pro Val
 340 345 350
 Phe Gln Ala Arg Val Leu Gly His His His Gln Ala Gln Glu Thr Arg
 355 360 365
 Tyr Glu Val Arg Ile Gln Leu Val Tyr Lys Asn Arg Ser Pro Leu Arg
 370 375 380
 Ala Arg Glu Tyr Val Trp Ala Pro Gly His Cys Pro Cys Pro Met Leu
 385 390 395 400
 Ala Pro His Arg Asp Tyr Leu Met Ala Val Gln Arg Leu Val Ser Pro
 405 410 415
 Asp Gly Thr Gln Asp Gln Leu Leu Leu Pro His Ala Gly Tyr Ala Arg
 420 425 430
 Pro Trp Ser Pro Ala Glu Asp Ser Arg Ile Arg Leu Thr Ala Arg Arg
 435 440 445
 Cys Pro Gly
 450

<210> 51
 <211> 431
 <212> PRT

<213> homo sapiens

<400> 51

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Met Ile Arg Thr Pro Leu Ser Ala Ser Ala His Arg Leu Leu Leu Pro
 1           5           10           15
Gly Ser Arg Gly Arg Pro Pro Arg Asn Met Gln Pro Thr Gly Arg Glu
          20           25           30
Gly Ser Arg Ala Leu Ser Arg Arg Tyr Leu Arg Arg Leu Leu Leu Leu
          35           40           45
Leu Leu Leu Leu Leu Leu Arg Gln Pro Val Thr Arg Ala Glu Thr Thr
          50           55           60
Pro Gly Ala Pro Arg Ala Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe
65           70           75           80
Thr Thr Pro Gly Val Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr
          85           90           95
Pro Gly Thr Pro Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu
          100          105          110
Met Arg Ser Phe Pro Leu Val Asp Gly Tyr Val Gly Leu Asn Ser Ser
          115          120          125
Gln Lys Leu Ala Cys Leu Ile Gly Val Glu Gly Gly His Ser Leu Asp
          130          135          140
Ser Ser Leu Ser Val Leu Arg Ser Phe Tyr Val Leu Gly Val Arg Tyr
145          150          155          160
Leu Thr Leu Thr Phe Thr Cys Ser Thr Pro Trp Ala Glu Ser Ser Thr
          165          170          175
Lys Phe Arg His His Met Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe
          180          185          190
Gly Glu Lys Val Val Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp
          195          200          205
Leu Ser Tyr Ala Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser
210          215          220
Gln Ala Pro Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp
225          230          235          240
Asn Leu Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn
          245          250          255
Gly Gly Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn
          260          265          270
Leu Leu Ala Asn Val Ser Thr Val Ala Asp Asp Ser Asn Arg Cys Ser
          275          280          285
Val Pro Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp
          290          295          300
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr Pro
305          310          315          320
Val Leu Ile Glu Glu Leu Leu Ser Arg Ser Trp Ser Glu Glu Glu Leu
          325          330          335
Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg Gln Val Glu
          340          345          350
Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val Glu Ala Glu Phe
          355          360          365
Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser His Leu Val Pro Gln
370          375          380
Asn Gly His Gln Ala Thr His Leu Glu Val Thr Lys Gln Pro Thr Asn
385          390          395          400
Arg Val Pro Trp Arg Ser Ser Asn Ala Ser Pro Tyr Leu Val Pro Gly
          405          410          415
Leu Val Ala Ala Ala Thr Ile Pro Thr Phe Thr Gln Trp Leu Cys
          420          425          430

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<210> 52
 <211> 480
 <212> PRT
 <213> homo sapiens

<400> 52

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Met Gln Pro Ser Gly Leu Glu Gly Pro Gly Thr Phe Gly Arg Trp Pro
 1          5          10          15
Leu Leu Ser Leu Leu Leu Leu Leu Leu Gln Pro Val Thr Cys
          20          25          30
Ala Tyr Thr Thr Pro Gly Pro Pro Arg Ala Leu Thr Thr Leu Gly Ala
          35          40          45
Pro Arg Ala His Thr Met Pro Gly Thr Tyr Ala Pro Ser Thr Thr Leu
          50          55          60
Ser Ser Pro Ser Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met
65          70          75          80
Arg Asp Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu
          85          90          95
Arg Gln Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe
          100          105          110
Ser Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly
          115          120          125
Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg Asp
          130          135          140
Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg Met Cys
145          150          155          160
Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys Gly Leu Asn
          165          170          175
Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val Glu Gly Gly His Ser
          180          185          190
Leu Asp Ser Ser Leu Ser Val Leu Arg Ser Phe Tyr Val Leu Gly Val
          195          200          205
Arg Tyr Leu Thr Leu Thr Phe Thr Cys Ser Thr Pro Trp Ala Glu Ser
          210          215          220
Ser Thr Lys Phe Arg His His Met Tyr Thr Asn Val Ser Gly Leu Thr
225          230          235          240
Ser Phe Gly Glu Lys Val Val Glu Glu Leu Asn Arg Leu Gly Met Met
          245          250          255
Ile Asp Leu Ser Tyr Ala Ser Asp Thr Leu Ile Arg Arg Val Leu Glu
          260          265          270
Val Ser Gln Ala Pro Val Ile Phe Ser His Ser Ala Ala Arg Ala Val
          275          280          285
Cys Asp Asn Leu Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys
          290          295          300
Lys Asn Gly Gly Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln
305          310          315          320
Cys Asn Leu Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His
          325          330          335
Ile Arg Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr
          340          345          350
Asp Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr
          355          360          365
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Ser Trp Ser Glu Glu Glu
          370          375          380
Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg Gln Val
385          390          395          400
Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val Glu Ala Glu
          405          410          415
Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser His Leu Val Pro

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				420				425				430			
Gln	Asn	Gly	His	Gln	Ala	Thr	His	Leu	Glu	Val	Thr	Lys	Gln	Pro	Thr
				435				440				445			
Asn	Arg	Val	Pro	Trp	Arg	Ser	Ser	Asn	Ala	Ser	Pro	Tyr	Leu	Val	Pro
				450				455				460			
Gly	Leu	Val	Ala	Ala	Ala	Thr	Ile	Pro	Thr	Phe	Thr	Gln	Trp	Leu	Cys
				465				470				475			
												480			

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<210> 53
<211> 371
<212> PRT
<213> homo sapiens
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<400> 53															
Met	Asp	Ala	Ala	Thr	Ala	Pro	Lys	Gln	Ala	Trp	Pro	Pro	Trp	Pro	Pro
1				5					10					15	
Leu	Leu	Phe	Leu	Leu	Leu	Leu	Pro	Gly	Gly	Ser	Gly	Gly	Ser	Cys	Pro
		20						25					30		
Ala	Val	Cys	Asp	Cys	Thr	Ser	Gln	Pro	Gln	Ala	Val	Leu	Cys	Gly	His
		35					40					45			
Arg	Gln	Leu	Glu	Ala	Val	Pro	Gly	Gly	Leu	Pro	Leu	Asp	Thr	Glu	Leu
	50					55					60				
Leu	Asp	Leu	Ser	Gly	Asn	Arg	Leu	Pro	Lys	Ala	Gln	Pro	Leu	Val	Arg
65					70					75					80
Leu	Gln	Glu	Leu	Arg	Leu	Ser	Gly	Ala	Cys	Leu	Thr	Ser	Ile	Ala	Ala
				85					90					95	
His	Ala	Phe	His	Gly	Leu	Thr	Ala	Phe	His	Leu	Leu	Asp	Val	Ala	Asp
			100					105					110		
Asn	Ala	Leu	Gln	Thr	Leu	Glu	Glu	Thr	Ala	Phe	Pro	Ser	Pro	Asp	Lys
		115					120						125		
Leu	Val	Thr	Leu	Arg	Leu	Ser	Gly	Asn	Pro	Leu	Thr	Cys	Asp	Cys	Arg
	130					135						140			
Leu	Leu	Trp	Leu	Leu	Arg	Leu	Arg	His	Leu	Asp	Phe	Gly	Met	Ser	Pro
145					150					155					160
Pro	Ala	Cys	Ala	Gly	Pro	His	His	Val	Gln	Gly	Lys	Ser	Leu	Lys	Glu
				165					170					175	
Phe	Ser	Asp	Ile	Leu	Pro	Pro	Gly	His	Phe	Thr	Cys	Lys	Pro	Ala	Leu
			180					185					190		
Ile	Arg	Lys	Ser	Gly	Pro	Arg	Trp	Val	Ile	Ala	Glu	Glu	Gly	Gly	His
		195					200						205		
Ala	Val	Phe	Ser	Cys	Ser	Gly	Asp	Gly	Asp	Pro	Ala	Pro	Thr	Val	Ser
	210					215					220				
Trp	Met	Arg	Pro	His	Gly	Ala	Trp	Leu	Gly	Arg	Ala	Gly	Arg	Val	Arg
225				230						235				240	
Val	Leu	Glu	Asp	Gly	Thr	Leu	Glu	Ile	Arg	Ser	Val	Gln	Leu	Arg	Asp
				245					250					255	
Arg	Gly	Ala	Tyr	Val	Cys	Val	Val	Ser	Asn	Val	Ala	Gly	Asn	Asp	Ser
			260					265					270		
Leu	Arg	Thr	Trp	Leu	Glu	Val	Ile	Gln	Val	Glu	Pro	Pro	Asn	Gly	Thr
		275					280						285		
Leu	Ser	Asp	Pro	Asn	Ile	Thr	Val	Pro	Gly	Ile	Pro	Gly	Pro	Phe	Phe
	290					295					300				
Leu	Asp	Ser	Arg	Gly	Val	Ala	Met	Val	Leu	Ala	Val	Gly	Phe	Leu	Pro
305				310						315					320
Phe	Leu	Thr	Ser	Val	Thr	Leu	Cys	Phe	Gly	Leu	Ile	Ala	Leu	Trp	Ser
				325					330					335	
Lys	Gly	Lys	Gly	Arg	Val	Lys	His	His	Met	Thr	Phe	Asp	Phe	Val	Ala
			340					345					350		

Pro Arg Pro Ser Gly Asp Lys Asn Ser Gly Gly Asn Arg Val Thr Ala
 355 360 365
 Lys Leu Phe
 370

<210> 54
 <211> 592
 <212> PRT
 <213> homo sapiens

<400> 54
 Met Asp Ala Ala Thr Ala Pro Lys Gln Ala Trp Pro Pro Trp Pro Pro
 1 5 10 15
 Leu Leu Phe Leu Leu Leu Leu Pro Gly Gly Ser Gly Gly Ser Cys Pro
 20 25 30
 Ala Val Cys Asp Cys Thr Ser Gln Pro Gln Ala Val Leu Cys Gly His
 35 40 45
 Arg Gln Leu Glu Ala Val Pro Gly Gly Leu Pro Leu Asp Thr Glu Leu
 50 55 60
 Leu Asp Leu Ser Gly Asn Arg Leu Trp Gly Leu Gln Gln Gly Met Leu
 65 70 75 80
 Ser Arg Leu Ser Leu Leu Gln Glu Leu Asp Leu Ser Tyr Asn Gln Leu
 85 90 95
 Ser Thr Leu Glu Pro Gly Ala Phe His Gly Leu Gln Ser Leu Leu Thr
 100 105 110
 Leu Arg Leu Gln Gly Asn Arg Leu Arg Ile Met Gly Pro Gly Val Phe
 115 120 125
 Ser Gly Leu Ser Ala Leu Thr Leu Leu Asp Leu Arg Leu Asn Gln Ile
 130 135 140
 Val Leu Phe Leu Asp Gly Ala Phe Gly Glu Leu Gly Ser Leu Gln Lys
 145 150 155 160
 Leu Glu Val Gly Asp Asn His Leu Val Phe Val Ala Pro Gly Ala Phe
 165 170 175
 Ala Gly Leu Ala Lys Leu Ser Thr Leu Thr Leu Glu Arg Cys Asn Leu
 180 185 190
 Ser Thr Val Pro Gly Leu Ala Leu Ala Arg Leu Pro Ala Leu Val Ala
 195 200 205
 Leu Arg Leu Arg Glu Leu Asp Ile Gly Arg Leu Pro Ala Gly Ala Leu
 210 215 220
 Arg Gly Leu Gly Gln Leu Lys Glu Leu Glu Ile His Leu Trp Pro Ser
 225 230 235 240
 Leu Glu Ala Leu Asp Pro Gly Ser Leu Val Gly Leu Asn Leu Ser Ser
 245 250 255
 Leu Ala Ile Thr Arg Cys Asn Leu Ser Ser Val Pro Phe Gln Ala Leu
 260 265 270
 Tyr His Leu Ser Phe Leu Arg Val Leu Asp Leu Ser Gln Asn Pro Ile
 275 280 285
 Ser Ala Ile Pro Ala Arg Arg Leu Ser Pro Leu Val Arg Leu Gln Glu
 290 295 300
 Leu Arg Leu Ser Gly Ala Cys Leu Thr Ser Ile Ala Ala His Ala Phe
 305 310 315 320
 His Gly Leu Thr Ala Phe His Leu Leu Asp Val Ala Asp Asn Ala Leu
 325 330 335
 Gln Thr Leu Glu Glu Thr Ala Phe Pro Ser Pro Asp Lys Leu Val Thr
 340 345 350
 Leu Arg Leu Ser Gly Asn Pro Leu Thr Cys Asp Cys Arg Leu Leu Trp
 355 360 365
 Leu Leu Arg Leu Arg His Leu Asp Phe Gly Met Ser Pro Pro Ala Cys

370		375		380
Ala Gly Pro His His Val Gln Gly Lys Ser Leu Lys Glu Phe Ser Asp				
385		390		395
Ile Leu Pro Pro Gly His Phe Thr Cys Lys Pro Ala Leu Ile Arg Lys				400
	405		410	415
Ser Gly Pro Arg Trp Val Ile Ala Glu Glu Gly Gly His Ala Val Phe				
	420		425	430
Ser Cys Ser Gly Asp Gly Asp Pro Ala Pro Thr Val Ser Trp Met Arg				
	435		440	445
Pro His Gly Ala Trp Leu Gly Arg Ala Gly Arg Val Arg Val Leu Glu				
	450		455	460
Asp Gly Thr Leu Glu Ile Arg Ser Val Gln Leu Arg Asp Arg Gly Ala				
465		470		475
Tyr Val Cys Val Val Ser Asn Val Ala Gly Asn Asp Ser Leu Arg Thr				
	485		490	495
Trp Leu Glu Val Ile Gln Val Glu Pro Asn Gly Thr Leu Ser Asp				
	500		505	510
Pro Asn Ile Thr Val Pro Gly Ile Pro Gly Pro Phe Phe Leu Asp Ser				
	515		520	525
Arg Gly Val Ala Met Val Leu Ala Val Gly Phe Leu Pro Phe Leu Thr				
	530		535	540
Ser Val Thr Leu Cys Phe Gly Leu Ile Ala Leu Trp Ser Lys Gly Lys				
545		550		555
Gly Arg Val Lys His His Met Thr Phe Asp Phe Val Ala Pro Arg Pro				
	565		570	575
Ser Gly Asp Lys Asn Ser Gly Gly Asn Arg Val Thr Ala Lys Leu Phe				
	580		585	590

<210> 55

<211> 142

<212> PRT

<213> homo sapiens

<400> 55

Met Ala Arg Tyr Met Leu Leu Leu Leu Leu Ala Val Trp Val Leu Thr		
1	5	10
Gly Glu Leu Trp Pro Gly Ala Glu Ala Arg Ala Ala Pro Tyr Gly Val		
	20	25
Arg Leu Cys Gly Arg Glu Phe Ile Arg Ala Val Ile Phe Thr Cys Gly		
	35	40
Gly Ser Arg Trp Arg Arg Ser Asp Ile Leu Ala His Glu Ala Met Gly		
	50	55
Asp Thr Phe Pro Asp Ala Asp Ala Asp Glu Asp Ser Leu Ala Gly Glu		
65	70	75
Leu Asp Glu Ala Met Gly Ser Ser Glu Trp Leu Ala Leu Thr Lys Ser		
	85	90
Pro Gln Ala Phe Tyr Arg Gly Arg Pro Ser Trp Gln Gly Thr Pro Gly		
	100	105
Val Leu Arg Gly Ser Arg Asp Val Leu Ala Gly Leu Ser Ser Ser Cys		
	115	120
Cys Lys Trp Gly Cys Ser Lys Ser Glu Ile Ser Ser Leu Cys		
	130	135
		140

<210> 56

<211> 230

<212> PRT

<213> homo sapiens

<400> 56

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Met Ser Glu Glu Val Thr Tyr Ala Thr Leu Thr Phe Gln Asp Ser Ala
 1          5          10          15
Gly Ala Arg Asn Asn Arg Asp Gly Asn Asn Leu Arg Lys Arg Gly His
          20          25          30
Pro Ala Pro Ser Pro Ile Trp Arg His Ala Ala Leu Gly Leu Val Thr
          35          40          45
Leu Cys Leu Met Leu Leu Ile Gly Leu Val Thr Leu Gly Met Met Phe
          50          55          60
Leu Gln Ile Ser Asn Asp Ile Asn Ser Asp Ser Glu Lys Leu Ser Gln
65          70          75          80
Leu Gln Lys Thr Ile Gln Gln Gln Gln Asp Asn Leu Ser Gln Gln Leu
          85          90          95
Gly Asn Ser Asn Asn Leu Ser Met Glu Glu Glu Phe Leu Lys Ser Gln
          100          105          110
Ile Ser Ser Leu Leu Lys Arg Gln Glu Gln Met Ala Ile Lys Leu Cys
          115          120          125
Gln Glu Leu Ile Ile His Thr Ser Asp His Arg Cys Asn Pro Cys Pro
          130          135          140
Lys Met Trp Gln Trp Tyr Gln Asn Ser Cys Tyr Tyr Phe Thr Thr Asn
145          150          155          160
Glu Glu Lys Thr Trp Ala Asn Ser Arg Lys Asp Cys Ile Asp Lys Asn
          165          170          175
Ser Thr Leu Val Lys Ile Asp Ser Leu Glu Glu Lys Asp Phe Leu Met
          180          185          190
Ser Gln Pro Leu Leu Met Phe Ser Phe Phe Trp Leu Gly Leu Ser Trp
          195          200          205
Asp Ser Ser Gly Arg Ser Trp Phe Trp Glu Asp Gly Ser Val Pro Ser
          210          215          220
Pro Ser Leu Tyr Val Ser
225          230

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<210> 57

<211> 194

<212> PRT

<213> homo sapiens

<400> 57

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Met Trp Leu Ser Pro Ala Leu Leu Leu Leu Ile Leu Pro Gly Tyr Ser
 1          5          10          15
Ile Ala Ala Lys Ile Thr Gly Pro Thr Thr Val Asn Gly Ser Glu Gln
          20          25          30
Gly Ser Leu Thr Val Gln Cys Ala Tyr Gly Ser Gly Trp Glu Thr Tyr
          35          40          45
Leu Lys Trp Arg Cys Gln Gly Ala Asp Trp Asn Tyr Cys Asn Ile Leu
          50          55          60
Val Lys Thr Asn Gly Ser Glu Gln Glu Val Lys Lys Asn Arg Val Ser
65          70          75          80
Ile Arg Asp Asn Gln Lys Asn His Met Phe Thr Val Thr Met Glu Asn
          85          90          95
Leu Lys Arg Asp Asp Ala Asp Ser Tyr Trp Cys Gly Thr Glu Arg Pro
          100          105          110
Gly Ile Asp Leu Gly Val Lys Val Gln Val Thr Ile Asn Pro Gly Thr
          115          120          125
Gln Thr Ala Val Ser Glu Trp Thr Thr Thr Thr Ala Ser Leu Ala Phe
          130          135          140
Thr Ala Ala Ala Thr Gln Lys Thr Ser Ser Pro Leu Thr Arg Ser Pro

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145 150 155 160
 Leu Lys Ser Thr His Phe Leu Phe Leu Phe Leu Leu Glu Leu Pro Leu
 165 170 175
 Leu Leu Ser Met Leu Gly Thr Val Leu Trp Val Asn Arg Pro Gln Arg
 180 185 190
 Arg Ser

<210> 58

<211> 333

<212> PRT

<213> homo sapiens

<400> 58

Met Arg Ile Trp Trp Leu Leu Leu Ala Ile Glu Ile Cys Thr Gly Asn
 1 5 10 15
 Ile Asn Ser Gln Asp Thr Cys Arg Gln Gly His Pro Gly Ile Pro Gly
 20 25 30
 Asn Pro Gly His Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Ala
 35 40 45
 Lys Gly Asp Lys Gly Asp Ala Gly Glu Pro Gly Arg Pro Gly Ser Pro
 50 55 60
 Gly Lys Asp Gly Thr Ser Gly Glu Lys Gly Glu Arg Gly Ala Asp Gly
 65 70 75 80
 Lys Val Glu Ala Lys Gly Ile Lys Gly Asp Gln Gly Ser Arg Gly Ser
 85 90 95
 Pro Gly Lys His Gly Pro Lys Gly Leu Ala Gly Pro Met Gly Glu Lys
 100 105 110
 Gly Leu Arg Gly Glu Thr Gly Pro Gln Gly Gln Lys Gly Asn Lys Gly
 115 120 125
 Asp Val Gly Pro Thr Gly Pro Glu Gly Pro Arg Gly Asn Ile Gly Pro
 130 135 140
 Leu Gly Pro Thr Gly Leu Pro Gly Pro Met Gly Pro Ile Gly Lys Pro
 145 150 155 160
 Gly Pro Lys Gly Glu Ala Gly Pro Thr Gly Pro Gln Gly Glu Pro Gly
 165 170 175
 Val Arg Gly Ile Arg Gly Trp Lys Gly Asp Arg Gly Glu Lys Gly Lys
 180 185 190
 Ile Gly Glu Thr Leu Val Leu Pro Lys Ser Ala Phe Thr Val Gly Leu
 195 200 205
 Thr Val Leu Ser Lys Phe Pro Ser Ser Asp Met Pro Ile Lys Phe Asp
 210 215 220
 Lys Ile Leu Tyr Asn Glu Phe Asn His Tyr Asp Thr Ala Ala Gly Lys
 225 230 235 240
 Phe Thr Cys His Ile Ala Gly Val Tyr Tyr Phe Thr Tyr His Ile Thr
 245 250 255
 Val Phe Ser Arg Asn Val Gln Val Ser Leu Val Lys Asn Gly Val Lys
 260 265 270
 Ile Leu His Thr Lys Asp Ala Tyr Met Ser Ser Glu Asp Gln Ala Ser
 275 280 285
 Gly Gly Ile Val Leu Gln Leu Lys Leu Gly Asp Glu Val Trp Leu Gln
 290 295 300
 Val Thr Gly Gly Glu Arg Phe Asn Gly Leu Phe Ala Asp Glu Asp Asp
 305 310 315 320
 Asp Thr Thr Phe Thr Gly Phe Leu Leu Phe Ser Ser Pro
 325 330

<210> 59
 <211> 225
 <212> PRT
 <213> homo sapiens

<400> 59
 Met Arg Ile Trp Trp Leu Leu Leu Ala Ile Glu Ile Cys Thr Gly Asn
 1 5 10 15
 Ile Asn Ser Gln Asp Thr Cys Arg Gln Gly His Pro Gly Ile Pro Gly
 20 25 30
 Asn Pro Gly His Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Ala
 35 40 45
 Lys Gly Asp Lys Gly Asp Ala Gly Glu Ala Gly Pro Thr Gly Pro Gln
 50 55 60
 Gly Glu Pro Gly Val Arg Gly Ile Arg Gly Trp Lys Gly Asp Arg Gly
 65 70 75 80
 Glu Lys Gly Lys Ile Gly Glu Thr Leu Val Leu Pro Lys Ser Ala Phe
 85 90 95
 Thr Val Gly Leu Thr Val Leu Ser Lys Phe Pro Ser Ser Asp Met Pro
 100 105 110
 Ile Lys Phe Asp Lys Ile Leu Tyr Asn Glu Phe Asn His Tyr Asp Thr
 115 120 125
 Ala Ala Gly Lys Phe Thr Cys His Ile Ala Gly Val Tyr Tyr Phe Thr
 130 135 140
 Tyr His Ile Thr Val Phe Ser Arg Asn Val Gln Val Ser Leu Val Lys
 145 150 155 160
 Asn Gly Val Lys Ile Leu His Thr Lys Asp Ala Tyr Met Ser Ser Glu
 165 170 175
 Asp Gln Ala Ser Gly Gly Ile Val Leu Gln Leu Lys Leu Gly Asp Glu
 180 185 190
 Val Trp Leu Gln Val Thr Gly Gly Glu Arg Phe Asn Gly Leu Phe Ala
 195 200 205
 Asp Glu Asp Asp Asp Thr Thr Phe Thr Gly Phe Leu Leu Phe Ser Ser
 210 215 220
 Pro
 225

<210> 60
 <211> 205
 <212> PRT
 <213> homo sapiens

<400> 60
 Met Met Arg Thr Leu Ile Thr Thr His Pro Leu Pro Leu Leu Leu Leu
 1 5 10 15
 Pro Gln Gln Leu Leu Gln Leu Val Gln Phe Gln Glu Val Asp Thr Asp
 20 25 30
 Phe Asp Phe Pro Glu Glu Asp Lys Lys Glu Glu Phe Glu Glu Cys Leu
 35 40 45
 Glu Lys Phe Phe Ser Thr Gly Pro Ala Arg Pro Pro Thr Lys Glu Lys
 50 55 60
 Val Lys Arg Arg Val Leu Ile Glu Pro Gly Met Pro Leu Asn His Ile
 65 70 75 80
 Glu Tyr Cys Asn His Glu Ile Met Gly Lys Asn Val Tyr Tyr Lys His
 85 90 95
 Arg Trp Val Ala Glu His Tyr Phe Leu Leu Met Gln Tyr Asp Glu Leu
 100 105 110
 Gln Lys Ile Cys Tyr Asn Arg Phe Val Pro Cys Lys Asn Gly Ile Arg

<400>	62															
Met	Glu	Val	Gly	Met	Gly	Cys	Trp	Ala	Arg	Glu	Val	Leu	Val	Pro	Glu	
1				5					10					15		
Gly	Pro	Leu	Tyr	Arg	Val	Ala	Gly	Thr	Ala	Val	Ser	Ile	Ser	Cys	Asn	
			20					25					30			
Val	Thr	Gly	Tyr	Glu	Gly	Pro	Ala	Gln	Gln	Asn	Phe	Glu	Trp	Phe	Leu	
		35					40					45				
Tyr	Arg	Pro	Glu	Ala	Pro	Asp	Thr	Ala	Leu	Gly	Ile	Val	Ser	Thr	Lys	
	50					55					60					
Asp	Thr	Gln	Phe	Ser	Tyr	Ala	Val	Phe	Lys	Ser	Arg	Val	Val	Ala	Gly	
65					70					75					80	
Glu	Val	Gln	Val	Gln	Arg	Leu	Gln	Gly	Asp	Ala	Val	Val	Leu	Lys	Ile	
				85					90					95		
Ala	Arg	Leu	Gln	Ala	Gln	Asp	Ala	Gly	Ile	Tyr	Glu	Cys	His	Thr	Pro	
			100					105					110			
Ser	Thr	Asp	Thr	Arg	Tyr	Leu	Gly	Ser	Tyr	Ser	Gly	Lys	Val	Glu	Leu	
		115					120					125				
Arg	Val	Leu	Pro	Asp	Val	Leu	Gln	Val	Ser	Ala	Ala	Pro	Pro	Gly	Pro	
	130					135					140					
Arg	Gly	Arg	Gln	Ala	Pro	Thr	Ser	Pro	Pro	Arg	Met	Thr	Val	His	Glu	
145					150					155					160	

Gly Gln Glu Leu Ala Leu Gly Cys Leu Ala Arg Thr Ser Thr Gln Lys
 165 170 175
 His Thr His Leu Ala Val Ser Phe Gly Arg Ser Val Pro Glu Ala Pro
 180 185 190
 Val Gly Arg Ser Thr Leu Gln Glu Val Val Gly Ile Arg Ser Asp Leu
 195 200 205
 Ala Val Glu Ala Gly Ala Pro Tyr Ala Glu Arg Leu Ala Ala Gly Glu
 210 215 220
 Leu Arg Leu Gly Lys Glu Gly Thr Asp Arg Tyr Arg Met Val Val Gly
 225 230 235 240
 Gly Ala Gln Ala Gly Asp Ala Gly Thr Tyr His Cys Thr Ala Ala Glu
 245 250 255
 Trp Ile Gln Asp Pro Asp Gly Ser Trp Ala Gln Ile Ala Glu Lys Arg
 260 265 270
 Ala Val Leu Ala His Val Asp Val Gln Thr Leu Ser Ser Gln Leu Ala
 275 280 285
 Val Thr Val Gly Pro Gly Glu Arg Arg Ile Gly Pro Gly Glu Pro Leu
 290 295 300
 Glu Leu Leu Cys Asn Val Ser Gly Ala Leu Pro Pro Ala Gly Arg His
 305 310 315 320
 Ala Ala Tyr Ser Val Gly Trp Glu Met Ala Pro Ala Gly His Leu Gly
 325 330 335
 Pro Gly Arg Leu Val Ala Gln Leu Asp Thr Glu Gly Val Gly Ser Leu
 340 345 350
 Gly Pro Gly Tyr Glu Gly Arg His Ile Ala Met Glu Lys Val Ala Ser
 355 360 365
 Arg Thr Tyr Arg Leu Arg Leu Glu Ala Ala Arg Pro Gly Asp Ala Gly
 370 375 380
 Thr Tyr Arg Cys Leu Ala Lys Ala Tyr Val Arg Gly Ser Gly Thr Arg
 385 390 395 400
 Leu Arg Glu Ala Ala Ser Ala Arg Ser Arg Pro Leu Pro Val His Val
 405 410 415
 Arg Glu Glu Gly Val Val Leu Glu Ala Val Ala Trp Leu Ala Gly Gly
 420 425 430
 Thr Val Tyr Arg Gly Glu Thr Ala Ser Leu Leu Cys Asn Ile Ser Val
 435 440 445
 Arg Gly Gly Pro Pro Gly Leu Arg Leu Ala Ala Ser Trp Trp Val Glu
 450 455 460
 Arg Pro Glu Asp Gly Glu Leu Ser Ser Val Pro Ala Gln Leu Val Gly
 465 470 475 480
 Gly Val Gly Gln Asp Gly Val Ala Glu Leu Gly Val Arg Pro Gly Gly
 485 490 495
 Gly Pro Val Ser Val Glu Leu Val Gly Pro Arg Ser His Arg Leu Arg
 500 505 510
 Leu His Ser Leu Gly Pro Glu Asp Glu Gly Val Tyr His Cys Ala Pro
 515 520 525
 Ser Ala Trp Val Gln His Ala Asp Tyr Ser Trp Tyr Gln Ala Gly Ser
 530 535 540
 Ala Arg Ser Gly Pro Val Thr Val Tyr Pro Tyr Met His Ala Leu Asp
 545 550 555 560
 Thr Leu Phe Val Pro Leu Leu Val Gly Thr Gly Val Ala Leu Val Thr
 565 570 575
 Gly Ala Thr Val Leu Gly Thr Ile Thr Cys Cys Phe Met Lys Arg Leu
 580 585 590
 Arg Lys Arg
 595

<211> 613

<212> PRT

<213> homo sapiens

<400> 63

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Met Gly Ala Leu Arg Pro Thr Leu Leu Pro Pro Ser Leu Pro Leu Leu
 1          5          10          15
Leu Leu Leu Met Leu Gly Met Gly Cys Trp Ala Arg Glu Val Leu Val
 20          25          30
Pro Glu Gly Pro Leu Tyr Arg Val Ala Gly Thr Ala Val Ser Ile Ser
 35          40          45
Cys Asn Val Thr Gly Tyr Glu Gly Pro Ala Gln Gln Asn Phe Glu Trp
 50          55          60
Phe Leu Tyr Arg Pro Glu Ala Pro Asp Thr Ala Leu Gly Ile Val Ser
 65          70          75          80
Thr Lys Asp Thr Gln Phe Ser Tyr Ala Val Phe Lys Ser Arg Val Val
 85          90          95
Ala Gly Glu Val Gln Val Gln Arg Leu Gln Gly Asp Ala Val Val Leu
100          105          110
Lys Ile Ala Arg Leu Gln Ala Gln Asp Ala Gly Ile Tyr Glu Cys His
115          120          125
Thr Pro Ser Thr Asp Thr Arg Tyr Leu Gly Ser Tyr Ser Gly Lys Val
130          135          140
Glu Leu Arg Val Leu Pro Asp Val Leu Gln Val Ser Ala Ala Pro Pro
145          150          155          160
Gly Pro Arg Gly Arg Gln Ala Pro Thr Ser Pro Pro Arg Met Thr Val
165          170          175
His Glu Gly Gln Glu Leu Ala Leu Gly Cys Leu Ala Arg Thr Ser Thr
180          185          190
Gln Lys His Thr His Leu Ala Val Ser Phe Gly Arg Ser Val Pro Glu
195          200          205
Ala Pro Val Gly Arg Ser Thr Leu Gln Glu Val Val Gly Ile Arg Ser
210          215          220
Asp Leu Ala Val Glu Ala Gly Ala Pro Tyr Ala Glu Arg Leu Ala Ala
225          230          235          240
Gly Glu Leu Arg Leu Gly Lys Glu Gly Thr Asp Arg Tyr Arg Met Val
245          250          255
Val Gly Gly Ala Gln Ala Gly Asp Ala Gly Thr Tyr His Cys Thr Ala
260          265          270
Ala Glu Trp Ile Gln Asp Pro Asp Gly Ser Trp Ala Gln Ile Ala Glu
275          280          285
Lys Arg Ala Val Leu Ala His Val Asp Val Gln Thr Leu Ser Ser Gln
290          295          300
Leu Ala Val Thr Val Gly Pro Gly Glu Arg Arg Ile Gly Pro Gly Glu
305          310          315          320
Pro Leu Glu Leu Leu Cys Asn Val Ser Gly Ala Leu Pro Pro Ala Gly
325          330          335
Arg His Ala Ala Tyr Ser Val Gly Trp Glu Met Ala Pro Ala Gly Ala
340          345          350
Pro Gly Pro Gly Arg Leu Val Ala Gln Leu Asp Thr Glu Gly Val Gly
355          360          365
Ser Leu Gly Pro Gly Tyr Glu Gly Arg His Ile Ala Met Glu Lys Val
370          375          380
Ala Ser Arg Thr Tyr Arg Leu Arg Leu Glu Ala Ala Arg Pro Gly Asp
385          390          395          400
Ala Gly Thr Tyr Arg Cys Leu Ala Lys Ala Tyr Val Arg Gly Ser Gly
405          410          415
Thr Arg Leu Arg Glu Ala Ala Ser Ala Arg Ser Arg Pro Leu Pro Val
420          425          430

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His Val Arg Glu Glu Gly Val Val Leu Glu Ala Val Ala Trp Leu Ala
 435 440 445
 Gly Gly Thr Val Tyr Arg Gly Glu Thr Ala Ser Leu Leu Cys Asn Ile
 450 455 460
 Ser Val Arg Gly Gly Pro Pro Gly Leu Arg Leu Ala Ala Ser Trp Trp
 465 470 475 480
 Val Glu Arg Pro Glu Asp Gly Glu Leu Ser Ser Val Pro Ala Gln Leu
 485 490 495
 Val Gly Gly Val Gly Gln Asp Gly Val Ala Glu Leu Gly Val Arg Pro
 500 505 510
 Gly Gly Gly Pro Val Ser Val Glu Leu Val Gly Pro Arg Ser His Arg
 515 520 525
 Leu Arg Leu His Ser Leu Gly Pro Glu Asp Glu Gly Val Tyr His Cys
 530 535 540
 Ala Pro Ser Ala Trp Val Gln His Ala Asp Tyr Ser Trp Tyr Gln Ala
 545 550 555 560
 Gly Ser Ala Arg Ser Gly Pro Val Thr Val Tyr Pro Tyr Met His Ala
 565 570 575
 Leu Asp Thr Leu Phe Val Pro Leu Leu Val Gly Thr Gly Val Ala Leu
 580 585 590
 Val Thr Gly Ala Thr Val Leu Gly Thr Ile Thr Cys Cys Phe Met Lys
 595 600 605
 Arg Leu Arg Lys Arg
 610

<210> 64

<211> 596

<212> PRT

<213> homo sapiens

<400> 64

Met Ala Ala Asn Ser Thr Ser Asp Leu His Thr Pro Gly Thr Gln Leu
 1 5 10 15
 Ser Val Ala Asp Ile Ile Val Ile Thr Val Tyr Phe Ala Leu Asn Val
 20 25 30
 Ala Val Gly Ile Trp Ser Ser Cys Arg Ala Ser Arg Asn Thr Val Asn
 35 40 45
 Gly Tyr Phe Leu Ala Gly Arg Asp Met Thr Trp Trp Pro Ile Gly Ala
 50 55 60
 Ser Leu Phe Ala Ser Ser Glu Gly Ser Gly Leu Phe Ile Gly Leu Ala
 65 70 75 80
 Gly Ser Gly Ala Ala Gly Gly Leu Ala Val Ala Gly Phe Glu Trp Asn
 85 90 95
 Ala Thr Tyr Val Leu Leu Ala Leu Ala Trp Val Phe Val Pro Ile Tyr
 100 105 110
 Ile Ser Ser Glu Ile Val Thr Leu Pro Glu Tyr Ile Gln Lys Arg Tyr
 115 120 125
 Gly Gly Gln Arg Ile Arg Met Tyr Leu Ser Val Leu Ser Leu Leu Leu
 130 135 140
 Ser Val Phe Thr Lys Ile Ser Leu Asp Leu Tyr Ala Gly Ala Leu Phe
 145 150 155 160
 Val His Ile Cys Leu Gly Trp Asn Phe Tyr Leu Ser Thr Ile Leu Thr
 165 170 175
 Leu Gly Ile Thr Ala Leu Tyr Thr Ile Ala Gly Gly Leu Ala Ala Val
 180 185 190
 Ile Tyr Thr Asp Ala Leu Gln Thr Leu Ile Met Val Val Gly Ala Val
 195 200 205
 Ile Leu Thr Ile Lys Ala Phe Asp Gln Ile Gly Gly Tyr Gly Gln Leu

210		215		220
Glu Ala Ala Tyr Ala Gln Ala Ile Pro Ser Arg Thr Ile Ala Asn Thr				
225		230		235
Thr Cys His Leu Pro Arg Thr Asp Ala Met His Met Phe Arg Asp Pro				240
	245		250	255
His Thr Gly Asp Leu Pro Trp Thr Gly Met Thr Phe Gly Leu Thr Ile				
	260		265	270
Met Ala Thr Trp Tyr Trp Cys Thr Asp Gln Val Ile Val Gln Arg Ser				
	275		280	285
Leu Ser Ala Arg Asp Leu Asn His Ala Lys Ala Gly Ser Ile Leu Ala				
	290		295	300
Ser Tyr Leu Lys Met Leu Pro Met Gly Leu Ile Ile Met Pro Gly Met				
305		310		315
Ile Ser Arg Ala Leu Phe Pro Asp Asp Val Gly Cys Val Val Pro Ser				
	325		330	335
Glu Cys Leu Arg Ala Cys Gly Ala Glu Val Gly Cys Ser Asn Ile Ala				
	340		345	350
Tyr Pro Lys Leu Val Met Glu Leu Met Pro Ile Gly Leu Arg Gly Leu				
	355		360	365
Met Ile Ala Val Met Leu Ala Ala Leu Met Ser Ser Leu Thr Ser Ile				
	370		375	380
Phe Asn Ser Ser Ser Thr Leu Phe Thr Met Asp Ile Trp Arg Arg Leu				
385		390		395
Arg Pro Arg Ser Gly Glu Arg Glu Leu Leu Val Gly Arg Leu Val				
	405		410	415
Ile Val Ala Leu Ile Gly Val Ser Val Ala Trp Ile Pro Val Leu Gln				
	420		425	430
Asp Ser Asn Ser Gly Gln Leu Phe Ile Tyr Met Gln Ser Val Thr Ser				
	435		440	445
Ser Leu Ala Pro Pro Val Thr Ala Val Phe Val Leu Gly Val Phe Trp				
	450		455	460
Arg Arg Ala Asn Glu Gln Gly Ala Phe Trp Gly Leu Ile Ala Gly Leu				
465		470		475
Val Val Gly Ala Thr Arg Leu Val Leu Glu Phe Leu Asn Pro Ala Pro				
	485		490	495
Pro Cys Gly Glu Pro Asp Thr Arg Pro Ala Val Leu Gly Ser Ile His				
	500		505	510
Tyr Leu His Phe Ala Val Ala Leu Phe Ala Leu Ser Gly Ala Val Val				
	515		520	525
Val Ala Gly Ser Leu Leu Thr Pro Pro Pro Gln Ser Val Gln Ile Glu				
	530		535	540
Asn Leu Thr Trp Trp Thr Leu Ala Gln Asp Val Pro Leu Gly Thr Lys				
545		550		555
Ala Gly Asp Gly Gln Thr Pro Gln Lys His Ala Phe Trp Ala Arg Val				
	565		570	575
Cys Gly Phe Asn Ala Ile Leu Leu Met Cys Val Asn Ile Phe Phe Tyr				
	580		585	590
Ala Tyr Phe Ala				
595				

<210> 65

<211> 393

<212> PRT

<213> homo sapiens

<400> 65

Met Asp Ser Leu Lys Asn Glu Asn Tyr Asp Leu Val Phe Val Glu Ala
1 5 10 15

Phe Asp Phe Cys Ser Phe Leu Ile Ala Glu Lys Leu Val Lys Pro Phe
 20 25 30
 Val Ala Ile Leu Pro Thr Thr Phe Gly Ser Leu Asp Phe Gly Leu Pro
 35 40 45
 Ser Pro Leu Ser Tyr Val Pro Val Phe Pro Ser Leu Leu Thr Asp His
 50 55 60
 Met Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe
 65 70 75 80
 Ser Arg Ser Gln Trp Asp Met Gln Ser Thr Phe Asp Asn Thr Ile Lys
 85 90 95
 Glu His Phe Pro Glu Gly Ser Arg Pro Val Leu Ser His Leu Leu Leu
 100 105 110
 Lys Ala Glu Leu Trp Phe Val Asn Ser Asp Phe Ala Phe Asp Phe Ala
 115 120 125
 Arg Pro Leu Leu Pro Asn Thr Val Tyr Ile Gly Gly Leu Met Glu Lys
 130 135 140
 Pro Ile Lys Pro Val Pro Gln Asp Leu Asp Asn Phe Ile Ala Asn Phe
 145 150 155 160
 Gly Asp Ala Gly Phe Val Leu Val Ala Phe Gly Ser Met Leu Asn Thr
 165 170 175
 His Gln Ser Gln Glu Val Leu Lys Lys Met His Asn Ala Phe Ala His
 180 185 190
 Leu Pro Gln Gly Val Ile Trp Thr Cys Gln Ser Ser His Trp Pro Arg
 195 200 205
 Asp Val His Leu Ala Thr Asn Val Lys Ile Val Asp Trp Leu Pro Gln
 210 215 220
 Ser Asp Leu Leu Ala His Pro Ser Ile Arg Leu Phe Val Thr His Gly
 225 230 235 240
 Gly Gln Asn Ser Val Met Glu Ala Ile Arg His Gly Val Pro Met Val
 245 250 255
 Gly Leu Pro Val Asn Gly Asp Gln His Gly Asn Met Val Arg Val Val
 260 265 270
 Ala Lys Asn Tyr Gly Val Ser Ile Arg Leu Asn Gln Val Thr Ala Asp
 275 280 285
 Thr Leu Thr Leu Thr Met Lys Gln Val Ile Glu Asp Lys Arg Tyr Lys
 290 295 300
 Ser Ala Val Val Ala Ala Ser Val Ile Leu His Ser Gln Pro Leu Ser
 305 310 315 320
 Pro Ala Gln Arg Leu Val Gly Trp Ile Asp His Ile Leu Gln Thr Gly
 325 330 335
 Gly Ala Thr His Leu Lys Pro Tyr Ala Phe Gln Gln Pro Trp His Glu
 340 345 350
 Gln Tyr Leu Ile Asp Val Phe Val Phe Leu Leu Gly Leu Thr Leu Gly
 355 360 365
 Thr Met Trp Leu Cys Gly Lys Leu Leu Gly Val Val Ala Arg Trp Leu
 370 375 380
 Arg Gly Ala Arg Lys Val Lys Lys Thr
 385 390

<210> 66

<211> 523

<212> PRT

<213> homo sapiens

<400> 66

Met Val Gly Gln Arg Val Leu Leu Leu Val Ala Phe Leu Leu Ser Gly
 1 5 10 15
 Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr Leu Gly

				20					25					30		
Gly	Ser	His	Tyr	Leu	Leu	Leu	Asp	Arg	Val	Ser	Gln	Ile	Leu	Gln	Glu	
		35					40					45				
His	Gly	His	Asn	Val	Thr	Met	Leu	His	Gln	Ser	Gly	Lys	Phe	Leu	Ile	
	50					55					60					
Pro	Asp	Ile	Lys	Glu	Glu	Glu	Lys	Ser	Tyr	Gln	Val	Ile	Arg	Trp	Phe	
65					70					75					80	
Ser	Pro	Glu	Asp	His	Gln	Lys	Arg	Ile	Lys	Lys	His	Phe	Asp	Ser	Tyr	
				85					90					95		
Ile	Glu	Thr	Ala	Leu	Asp	Gly	Arg	Lys	Glu	Ser	Glu	Ala	Leu	Val	Lys	
			100					105					110			
Leu	Met	Glu	Ile	Phe	Gly	Thr	Gln	Cys	Ser	Tyr	Leu	Leu	Ser	Arg	Lys	
		115					120					125				
Asp	Ile	Met	Asp	Ser	Leu	Lys	Asn	Glu	Asn	Tyr	Asp	Leu	Val	Phe	Val	
		130				135					140					
Glu	Ala	Phe	Asp	Phe	Cys	Ser	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Val	Lys	
145					150					155					160	
Pro	Phe	Val	Ala	Ile	Leu	Pro	Thr	Thr	Phe	Gly	Ser	Leu	Asp	Phe	Gly	
				165					170					175		
Leu	Pro	Ser	Pro	Leu	Ser	Tyr	Val	Pro	Val	Phe	Pro	Ser	Leu	Leu	Thr	
			180					185					190			
Asp	His	Met	Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	
		195					200					205				
Ser	Phe	Ser	Arg	Ser	Gln	Trp	Asp	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	
					215						220					
Ile	Lys	Glu	His	Phe	Pro	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu	
225					230					235					240	
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Val	Asn	Ser	Asp	Phe	Ala	Phe	Asp	
				245					250					255		
Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Ile	Gly	Gly	Leu	Met	
			260					265					270			
Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Asp	Asn	Phe	Ile	Ala	
						280						285				
Asn	Phe	Gly	Asp	Ala	Gly	Phe	Val	Leu	Val	Ala	Phe	Gly	Ser	Met	Leu	
						295					300					
Asn	Thr	His	Gln	Ser	Gln	Glu	Val	Leu	Lys	Lys	Met	His	Asn	Ala	Phe	
305					310					315					320	
Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Thr	Cys	Gln	Ser	Ser	His	Trp	
				325					330					335		
Pro	Arg	Asp	Val	His	Leu	Ala	Thr	Asn	Val	Lys	Ile	Val	Asp	Trp	Leu	
			340					345					350			
Pro	Gln	Ser	Asp	Leu	Leu	Ala	His	Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	
			355				360					36				

Leu Gly Thr Met Trp Leu Cys Gly Lys Leu Leu Gly Val Val Ala Arg
 500 505 510
 Trp Leu Arg Gly Ala Arg Lys Val Lys Lys Thr
 515 520

<210> 67
 <211> 252
 <212> PRT
 <213> homo sapiens

<400> 67
 Met Ser Cys Val Leu Gly Gly Val Ile Pro Leu Gly Leu Leu Phe Leu
 1 5 10 15
 Val Cys Gly Ser Gln Gly Tyr Leu Leu Pro Asn Val Thr Leu Leu Glu
 20 25 30
 Glu Leu Leu Ser Lys Tyr Gln His Asn Glu Ser His Ser Arg Val Arg
 35 40 45
 Arg Ala Ile Pro Arg Glu Asp Lys Glu Glu Ile Leu Met Leu His Asn
 50 55 60
 Lys Leu Arg Gly Gln Val Gln Pro Gln Ala Ser Asn Met Glu Tyr Met
 65 70 75 80
 Thr Trp Asp Asp Glu Leu Glu Lys Ser Ala Ala Ala Trp Ala Ser Gln
 85 90 95
 Cys Ile Trp Glu His Gly Pro Thr Ser Leu Leu Val Ser Ile Gly Gln
 100 105 110
 Asn Leu Gly Ala His Trp Gly Arg Tyr Arg Ser Pro Gly Phe His Val
 115 120 125
 Gln Ser Trp Tyr Asp Glu Val Lys Asp Tyr Thr Tyr Pro Tyr Pro Ser
 130 135 140
 Glu Cys Asn Pro Trp Cys Pro Glu Arg Cys Ser Gly Pro Met Cys Thr
 145 150 155 160
 His Tyr Thr Gln Ile Val Trp Ala Thr Thr Asn Lys Ile Gly Cys Ala
 165 170 175
 Val Asn Thr Cys Arg Lys Met Thr Val Trp Gly Glu Val Trp Glu Asn
 180 185 190
 Ala Val Tyr Phe Val Cys Asn Tyr Ser Pro Lys Gly Asn Trp Ile Gly
 195 200 205
 Glu Ala Pro Tyr Lys Asn Gly Arg Pro Cys Ser Glu Cys Pro Pro Ser
 210 215 220
 Tyr Gly Gly Ser Cys Arg Asn Asn Leu Cys Tyr Arg Gly Arg Lys Phe
 225 230 235 240
 Thr Pro Asn Thr Phe Ala Met Asn Leu Pro Ser Val
 245 250

<210> 68
 <211> 497
 <212> PRT
 <213> homo sapiens

<400> 68
 Met Ser Cys Val Leu Gly Gly Val Ile Pro Leu Gly Leu Leu Phe Leu
 1 5 10 15
 Val Cys Gly Ser Gln Gly Tyr Leu Leu Pro Asn Val Thr Leu Leu Glu
 20 25 30
 Glu Leu Leu Ser Lys Tyr Gln His Asn Glu Ser His Ser Arg Val Arg
 35 40 45
 Arg Ala Ile Pro Arg Glu Asp Lys Glu Glu Ile Leu Met Leu His Asn

50					55					60					
Lys	Leu	Arg	Gly	Gln	Val	Gln	Pro	Gln	Ala	Ser	Asn	Met	Glu	Tyr	Met
65					70					75					80
Thr	Trp	Asp	Asp	Glu	Leu	Glu	Lys	Ser	Ala	Ala	Ala	Trp	Ala	Ser	Gln
				85					90					95	
Cys	Ile	Trp	Glu	His	Gly	Pro	Thr	Ser	Leu	Leu	Val	Ser	Ile	Gly	Gln
			100					105					110		
Asn	Leu	Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Ser	Pro	Gly	Phe	His	Val
		115					120					125			
Gln	Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Tyr	Thr	Tyr	Pro	Tyr	Pro	Ser
	130					135					140				
Glu	Cys	Asn	Pro	Trp	Cys	Pro	Glu	Arg	Cys	Ser	Gly	Pro	Met	Cys	Thr
145					150					155					160
His	Tyr	Thr	Gln	Ile	Val	Trp	Ala	Thr	Thr	Asn	Lys	Ile	Gly	Cys	Ala
				165					170					175	
Val	Asn	Thr	Cys	Arg	Lys	Met	Thr	Val	Trp	Gly	Glu	Val	Trp	Glu	Asn
			180					185					190		
Ala	Val	Tyr	Phe	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly	Asn	Trp	Ile	Gly
		195					200					205			
Glu	Ala	Pro	Tyr	Lys	Asn	Gly	Arg	Pro	Cys	Ser	Glu	Cys	Pro	Pro	Ser
	210					215					220				
Tyr	Gly	Gly	Ser	Cys	Arg	Asn	Asn	Leu	Cys	Tyr	Arg	Glu	Glu	Thr	Tyr
225					230					235					240
Thr	Pro	Lys	Pro	Glu	Thr	Asp	Glu	Met	Asn	Glu	Val	Glu	Thr	Ala	Pro
				245					250					255	
Ile	Pro	Glu	Glu	Asn	His	Val	Trp	Leu	Gln	Pro	Arg	Val	Met	Arg	Pro
				260				265						270	
Thr	Lys	Pro	Lys	Lys	Thr	Ser	Ala	Val	Asn	Tyr	Met	Thr	Gln	Val	Val
		275					280						285		
Arg	Cys	Asp	Thr	Lys	Met	Lys	Asp	Arg	Cys	Lys	Gly	Ser	Thr	Cys	Asn
	290					295					300				
Arg	Tyr	Gln	Cys	Pro	Ala	Gly	Cys	Leu	Asn	His	Lys	Ala	Lys	Ile	Phe
305					310					315					320
Gly	Thr	Leu	Phe	Tyr	Glu	Ser	Ser	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Ile
				325					330					335	
His	Tyr	Gly	Ile	Leu	Asp	Asp	Lys	Gly	Gly	Leu	Val	Asp	Ile	Thr	Arg
			340					345					350		
Asn	Gly	Lys	Val	Pro	Phe	Phe	Val	Lys	Ser	Glu	Arg	His	Gly	Val	Gln
		355					360						365		
Ser	Leu	Ser	Lys	Tyr	Lys	Pro	Ser	Ser	Ser	Phe	Met	Val	Ser	Lys	Val
		370				375					380				
Lys	Val	Gln	Asp	Leu	Asp	Cys	Tyr	Thr	Thr	Val	Ala	Gln	Leu	Cys	Pro
385					390					395					400
Phe	Glu	Lys	Pro	Ala	Thr	His	Cys	Pro	Arg	Ile	His	Cys	Pro	Ala	His
				405					410					415	
Cys	Lys	Asp	Glu	Pro	Ser	Tyr	Trp	Ala	Pro	Val	Phe	Gly	Thr	Asn	Ile
			420					425					430		
Tyr	Ala	Asp	Thr	Ser	Ser	Ile	Cys	Lys	Thr	Ala	Val	His	Ala	Gly	Val
		435					440						445		
Ile	Ser	Asn	Glu	Ser	Gly	Gly	Asp	Val	Asp	Val	Met	Pro	Val	Asp	Lys
	450					455					460				
Lys	Lys	Thr	Tyr	Val	Gly	Ser	Leu	Arg	Asn	Gly	Val	Gln	Ser	Glu	Ser
465					470					475					480
Leu	Gly	Thr	Pro	Arg	Asp	Gly	Lys	Ala	Phe	Arg	Ile	Phe	Ala	Val	Arg
				485					490					495	

Gln

<210> 69

<211> 438

<212> PRT

<213> homo sapiens

<400> 69

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Asx Met Leu His Asn Lys Leu Arg Gly Gln Val Gln Pro Gln Ala Ser
 1          5          10          15
Asn Met Glu Tyr Met Thr Trp Asp Asp Glu Leu Glu Lys Ser Ala Ala
 20          25          30
Ala Trp Ala Ser Gln Cys Ile Trp Glu His Gly Pro Thr Ser Leu Leu
 35          40          45
Val Ser Ile Gly Gln Asn Leu Gly Ala His Trp Gly Arg Tyr Arg Ser
 50          55          60
Pro Gly Phe His Val Gln Ser Trp Tyr Asp Glu Val Lys Asp Tyr Thr
 65          70          75          80
Tyr Pro Tyr Pro Ser Glu Cys Asn Pro Trp Cys Pro Glu Arg Cys Ser
 85          90          95
Gly Pro Met Cys Thr His Tyr Thr Gln Ile Val Trp Ala Thr Thr Asn
100          105          110
Lys Ile Gly Cys Ala Val Asn Thr Cys Arg Lys Met Thr Val Trp Gly
115          120          125
Glu Val Trp Glu Asn Ala Val Tyr Phe Val Cys Asn Tyr Ser Pro Lys
130          135          140
Gly Asn Trp Ile Gly Glu Ala Pro Tyr Lys Asn Gly Arg Pro Cys Ser
145          150          155          160
Glu Cys Pro Pro Ser Tyr Gly Gly Ser Cys Arg Asn Asn Leu Cys Tyr
165          170          175
Arg Glu Glu Thr Tyr Thr Pro Lys Pro Glu Thr Asp Glu Met Asn Glu
180          185          190
Val Glu Thr Ala Pro Ile Pro Glu Glu Asn His Val Trp Leu Gln Pro
195          200          205
Arg Val Met Arg Pro Thr Lys Pro Lys Lys Thr Ser Ala Val Asn Tyr
210          215          220
Met Thr Gln Val Val Arg Cys Asp Thr Lys Met Lys Asp Arg Cys Lys
225          230          235          240
Gly Ser Thr Cys Asn Arg Tyr Gln Cys Pro Ala Gly Cys Leu Asn His
245          250          255
Lys Ala Lys Ile Phe Gly Thr Leu Phe Tyr Glu Ser Ser Ser Ser Ile
260          265          270
Cys Arg Ala Ala Ile His Tyr Gly Ile Leu Asp Asp Lys Gly Gly Leu
275          280          285
Val Asp Ile Thr Arg Asn Gly Lys Val Pro Phe Phe Val Lys Ser Glu
290          295          300
Arg His Gly Val Gln Ser Leu Ser Lys Tyr Lys Pro Ser Ser Ser Phe
305          310          315          320
Met Val Ser Lys Val Lys Val Gln Asp Leu Asp Cys Tyr Thr Thr Val
325          330          335
Ala Gln Leu Cys Pro Phe Glu Lys Pro Ala Thr His Cys Pro Arg Ile
340          345          350
His Cys Pro Ala His Cys Lys Asp Glu Pro Ser Tyr Trp Ala Pro Val
355          360          365
Phe Gly Thr Asn Ile Tyr Ala Asp Thr Ser Ser Ile Cys Lys Thr Ala
370          375          380
Val His Ala Gly Val Ile Ser Asn Glu Ser Gly Gly Asp Val Asp Val
385          390          395          400
Met Pro Val Asp Lys Lys Lys Thr Tyr Val Gly Ser Leu Arg Asn Gly
405          410          415
Val Gln Ser Glu Ser Leu Gly Thr Pro Arg Asp Gly Lys Ala Phe Arg

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420
Ile Phe Ala Val Arg Gln
435

425

430

<210> 70
<211> 308
<212> PRT
<213> homo sapiens

<400> 70
Met Val Gly Gly Val Leu Ala Ser Leu Gly Phe Val Phe Ser Ala Phe
1 5 10 15
Ala Ser Asp Leu Leu His Leu Tyr Leu Gly Leu Gly Leu Leu Ala Gly
20 25 30
Phe Gly Trp Ala Leu Val Phe Ala Pro Ala Leu Gly Thr Leu Ser Arg
35 40 45
Tyr Phe Ser Arg Arg Arg Val Leu Ala Val Gly Leu Ala Leu Thr Gly
50 55 60
Asn Gly Ala Ser Ser Leu Leu Leu Ala Pro Ala Leu Gln Leu Leu Leu
65 70 75 80
Asp Thr Phe Gly Trp Arg Gly Ala Leu Leu Leu Leu Gly Ala Ile Thr
85 90 95
Leu His Leu Thr Pro Cys Gly Ala Leu Leu Leu Pro Leu Val Leu Pro
100 105 110
Gly Asp Pro Pro Ala Pro Pro Arg Ser Pro Leu Ala Ala Leu Gly Leu
115 120 125
Ser Leu Phe Thr Arg Arg Ala Phe Ser Ile Phe Ala Leu Gly Thr Ala
130 135 140
Leu Val Gly Gly Gly Tyr Phe Val Pro Tyr Val His Leu Ala Pro His
145 150 155 160
Ala Leu Asp Arg Gly Leu Gly Gly Tyr Gly Ala Ala Leu Val Val Ala
165 170 175
Val Ala Ala Met Gly Asp Ala Gly Ala Arg Leu Val Cys Gly Trp Leu
180 185 190
Ala Asp Gln Gly Trp Val Pro Leu Pro Arg Leu Leu Ala Val Phe Gly
195 200 205
Ala Leu Thr Gly Leu Gly Leu Trp Val Val Gly Leu Val Pro Val Val
210 215 220
Gly Gly Glu Glu Ser Trp Gly Gly Pro Leu Leu Ala Ala Ala Val Ala
225 230 235 240
Tyr Gly Leu Ser Ala Gly Ser Tyr Ala Pro Leu Val Phe Gly Val Leu
245 250 255
Pro Gly Leu Val Gly Val Gly Gly Val Val Gln Ala Thr Gly Leu Val
260 265 270
Met Met Leu Met Ser Leu Gly Gly Leu Leu Gly Pro Pro Leu Ser Gly
275 280 285
Lys Asp Leu Ser Ser Gln Ile Cys Leu Gln Leu Ser Ser Ala Pro Gly
290 295 300
Val Arg Gly Phe
305

<210> 71
<211> 447
<212> PRT
<213> homo sapiens

<400> 71

```

Met Thr Pro Gln Pro Ala Gly Pro Pro Asp Gly Gly Trp Gly Trp Val
 1      5      10      15
Val Ala Ala Ala Phe Ala Ile Asn Gly Leu Ser Tyr Gly Leu Leu
 20      25      30
Arg Ser Leu Gly Leu Ala Phe Pro Asp Leu Ala Glu His Phe Asp Arg
 35      40      45
Ser Ala Gln Asp Thr Ala Trp Ile Ser Ala Leu Ala Leu Ala Val Gln
 50      55      60
Gln Ala Ala Ser Pro Val Gly Ser Ala Leu Ser Thr Arg Trp Gly Ala
 65      70      75      80
Arg Pro Val Val Met Val Gly Gly Val Leu Ala Ser Leu Gly Phe Val
 85      90      95
Phe Ser Ala Phe Ala Ser Asp Leu Leu His Leu Tyr Leu Gly Leu Gly
100      105      110
Leu Leu Ala Gly Phe Gly Trp Ala Leu Val Phe Ala Pro Ala Leu Gly
115      120      125
Thr Leu Ser Arg Tyr Phe Ser Arg Arg Arg Val Leu Ala Val Gly Leu
130      135      140
Ala Leu Thr Gly Asn Gly Ala Ser Ser Leu Leu Leu Ala Pro Ala Leu
145      150      155      160
Gln Leu Leu Leu Asp Thr Phe Gly Trp Arg Gly Ala Leu Leu Leu Leu
165      170      175
Gly Ala Ile Thr Leu His Leu Thr Pro Cys Gly Ala Leu Leu Leu Pro
180      185      190
Leu Val Leu Pro Gly Asp Pro Pro Ala Pro Pro Arg Ser Pro Leu Ala
195      200      205
Ala Leu Gly Leu Ser Leu Phe Thr Arg Arg Ala Phe Ser Ile Phe Ala
210      215      220
Leu Gly Thr Ala Leu Val Gly Gly Gly Tyr Phe Val Pro Tyr Val His
225      230      235      240
Leu Ala Pro His Ala Leu Asp Arg Gly Leu Gly Gly Tyr Gly Ala Ala
245      250      255
Leu Val Val Ala Val Ala Ala Met Gly Asp Ala Gly Ala Arg Leu Val
260      265      270
Cys Gly Trp Leu Ala Asp Gln Gly Trp Val Pro Leu Pro Arg Leu Leu
275      280      285
Ala Val Phe Gly Ala Leu Thr Gly Leu Gly Leu Trp Val Val Gly Leu
290      295      300
Val Pro Val Val Gly Gly Glu Glu Ser Trp Gly Gly Pro Leu Leu Ala
305      310      315      320
Ala Ala Val Ala Tyr Gly Leu Ser Ala Gly Ser Tyr Ala Pro Leu Val
325      330      335
Phe Gly Val Leu Pro Gly Leu Val Gly Val Gly Gly Val Val Gln Ala
340      345      350
Thr Gly Leu Val Met Met Leu Met Ser Leu Gly Gly Leu Leu Gly Pro
355      360      365
Pro Leu Ser Gly Phe Leu Arg Asp Glu Thr Gly Asp Phe Thr Ala Ser
370      375      380
Phe Leu Leu Ser Gly Ser Leu Ile Leu Ser Gly Ser Phe Ile Tyr Ile
385      390      395      400
Gly Leu Pro Arg Ala Leu Pro Ser Cys Gly Pro Ala Ser Pro Pro Ala
405      410      415
Thr Pro Pro Pro Glu Thr Gly Glu Leu Leu Pro Ala Pro Gln Ala Val
420      425      430
Leu Leu Ser Pro Gly Gly Pro Gly Ser Thr Leu Asp Thr Thr Cys
435      440      445

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<211> 458

<212> PRT

<213> homo sapiens

<400> 72

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Asx Met Ala Arg Arg Thr Glu Pro Pro Asp Gly Gly Trp Gly Trp Val
 1          5          10          15
Val Val Leu Ser Ala Phe Phe Gln Ser Ala Leu Val Phe Gly Val Leu
      20          25          30
Arg Ser Phe Gly Val Phe Phe Val Glu Phe Val Ala Ala Phe Glu Glu
      35          40          45
Gln Ala Ala Arg Val Ser Trp Ile Ala Ser Ile Gly Ile Ala Val Gln
      50          55          60
Gln Phe Gly Ser Pro Val Gly Ser Ala Leu Ser Thr Lys Phe Gly Pro
65          70          75          80
Arg Pro Val Val Met Thr Gly Gly Ile Leu Ala Ala Leu Gly Met Leu
      85          90          95
Leu Ala Ser Phe Ala Thr Ser Leu Thr His Leu Tyr Leu Ser Ile Gly
      100          105          110
Leu Leu Ser Gly Ser Gly Trp Ala Leu Thr Phe Ala Pro Thr Leu Ala
      115          120          125
Cys Leu Ser Cys Tyr Phe Ser Arg Arg Arg Ser Leu Ala Thr Gly Leu
      130          135          140
Ala Leu Thr Gly Val Gly Leu Ser Ser Phe Thr Phe Ala Pro Phe Phe
145          150          155          160
Gln Trp Leu Leu Ser His Tyr Ala Trp Arg Gly Ser Leu Leu Leu Val
      165          170          175
Ser Ala Leu Ser Leu His Leu Val Ala Cys Gly Ala Leu Leu Arg Pro
      180          185          190
Pro Ser Leu Ala Glu Asp Pro Ala Val Gly Gly Pro Arg Ala Gln Leu
      195          200          205
Thr Ser Leu Leu His His Gly Pro Phe Leu Arg Tyr Thr Val Ala Leu
      210          215          220
Thr Leu Ile Asn Thr Gly Tyr Phe Ile Pro Tyr Leu His Leu Val Ala
225          230          235          240
His Leu Gln Asp Leu Asp Trp Asp Pro Leu Pro Ala Ala Phe Leu Leu
      245          250          255
Ser Val Val Ala Ile Ser Asp Leu Val Gly Arg Val Val Ser Gly Trp
      260          265          270
Leu Gly Asp Ala Val Pro Gly Pro Val Thr Arg Leu Leu Met Leu Trp
      275          280          285
Thr Thr Leu Thr Gly Val Ser Leu Ala Leu Phe Pro Val Ala Gln Ala
      290          295          300
Pro Thr Ala Leu Val Ala Leu Ala Val Ala Tyr Gly Phe Thr Ser Gly
305          310          315          320
Ala Leu Ala Pro Leu Ala Phe Ser Val Leu Pro Glu Leu Ile Gly Thr
      325          330          335
Arg Arg Ile Tyr Cys Gly Leu Gly Leu Leu Gln Met Ile Glu Ser Ile
      340          345          350
Gly Gly Leu Leu Gly Pro Pro Leu Ser Gly Tyr Leu Arg Asp Val Ser
      355          360          365
Gly Asn Tyr Thr Ala Ser Phe Val Val Ala Gly Ala Phe Leu Leu Ser
      370          375          380
Gly Ser Gly Ile Leu Leu Thr Leu Pro His Phe Phe Cys Phe Ser Thr
385          390          395          400
Thr Thr Ser Gly Pro Gln Asp Leu Val Thr Glu Ala Leu Asp Thr Lys
      405          410          415
Val Pro Leu Pro Lys Glu Gly Leu Glu Gly Gly Leu Asn Ser Thr Glu
      420          425          430

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Ser Gly Pro Glu Ser Gln Ser Leu Thr Ala Pro Gly Leu Leu Leu Pro
 435 440 445
 Arg Leu Gly Leu His Arg Thr Thr Val Pro
 450 455

<210> 73
 <211> 169
 <212> PRT
 <213> homo sapiens

<400> 73
 Met Thr Met Lys Thr Ser Gly Ala Thr Cys Asp Ala Asn Ser Val Met
 1 5 10 15
 Asn Cys Gly Ile Arg Gly Ser Glu Met Phe Ala Glu Met Asp Leu Arg
 20 25 30
 Ala Ile Lys Pro Tyr Gln Thr Leu Ile Lys Lys Val Gly Gln Arg His
 35 40 45
 Cys Val Asp Pro Ala Val Ile Ala Ala Ile Ile Ser Arg Glu Ser His
 50 55 60
 Gly Gly Ser Val Leu Gln Asp Gly Trp Asp His Arg Gly Leu Lys Phe
 65 70 75 80
 Gly Leu Met Gln Leu Asp Lys Gln Thr Tyr His Pro Val Gly Ala Trp
 85 90 95
 Asp Ser Lys Glu His Leu Ser Gln Ala Thr Gly Ile Leu Thr Glu Arg
 100 105 110
 Ile Lys Ala Ile Gln Lys Lys Phe Pro Thr Trp Ser Val Ala Gln His
 115 120 125
 Leu Lys Gly Gly Leu Ser Ala Phe Lys Ser Gly Ile Glu Ala Ile Ala
 130 135 140
 Thr Pro Ser Asp Ile Asp Asn Asp Phe Val Asn Asp Ile Ile Ala Arg
 145 150 155 160
 Ala Lys Phe Tyr Lys Arg Gln Ser Phe
 165

<210> 74
 <211> 186
 <212> PRT
 <213> homo sapiens

<400> 74
 Met Lys Pro His Leu His Pro Arg Leu Tyr His Gly Cys Tyr Gly Asp
 1 5 10 15
 Ile Met Thr Met Lys Thr Ser Gly Ala Thr Cys Asp Ala Asn Ser Val
 20 25 30
 Met Asn Cys Gly Ile Arg Gly Ser Glu Met Phe Ala Glu Met Asp Leu
 35 40 45
 Arg Ala Ile Lys Pro Tyr Gln Thr Leu Ile Lys Lys Val Gly Gln Arg
 50 55 60
 His Cys Val Asp Pro Ala Val Ile Ala Ala Ile Ile Ser Arg Glu Ser
 65 70 75 80
 His Gly Gly Ser Val Leu Gln Asp Gly Trp Asp His Arg Gly Leu Lys
 85 90 95
 Phe Gly Leu Met Gln Leu Asp Lys Gln Thr Tyr His Pro Val Gly Ala
 100 105 110
 Trp Asp Ser Lys Glu His Leu Ser Gln Ala Thr Gly Ile Leu Thr Glu
 115 120 125
 Arg Ile Lys Ala Ile Gln Lys Lys Phe Pro Thr Trp Ser Val Ala Gln

130		135		140
His Leu Lys Gly Gly Leu Ser Ala Phe Lys Ser Gly Ile Glu Ala Ile				
145		150		155
Ala Thr Pro Ser Asp Ile Asp Asn Asp Phe Val Asn Asp Ile Ile Ala				
	165		170	175
Arg Ala Lys Phe Tyr Lys Arg Gln Ser Phe				
	180		185	

<210> 75

<211> 675

<212> PRT

<213> homo sapiens

<400> 75

Met Glu Ser Gly Thr Ser Ser Pro Gln Pro Pro Gln Leu Asp Pro Leu				
1	5		10	15
Asp Ala Phe Pro Gln Lys Gly Leu Glu Pro Gly Asp Ile Ala Val Leu				
	20		25	30
Val Leu Tyr Phe Leu Phe Val Leu Ala Val Gly Leu Trp Ser Thr Val				
	35		40	45
Lys Thr Lys Arg Asp Thr Val Lys Gly Tyr Phe Leu Ala Gly Gly Asp				
	50		55	60
Met Val Trp Trp Pro Val Gly Ala Ser Leu Phe Ala Ser Asn Val Gly				
	65		70	75
Ser Gly His Phe Ile Gly Leu Ala Gly Ser Gly Ala Ala Thr Gly Ile				
	85		90	95
Ser Val Ser Ala Tyr Glu Leu Asn Gly Leu Phe Ser Val Leu Met Leu				
	100		105	110
Ala Trp Ile Phe Leu Pro Ile Tyr Ile Ala Gly Gln Val Thr Thr Met				
	115		120	125
Pro Glu Tyr Leu Arg Lys Arg Phe Gly Gly Ile Arg Ile Pro Ile Ile				
	130		135	140
Leu Ala Val Leu Tyr Leu Phe Ile Tyr Ile Phe Thr Lys Ile Ser Val				
	145		150	155
Asp Met Tyr Ala Gly Ala Ile Phe Ile Gln Gln Ser Leu His Leu Asp				
	165		170	175
Leu Tyr Leu Ala Ile Val Gly Leu Leu Ala Ile Thr Ala Val Tyr Thr				
	180		185	190
Val Ala Gly Gly Leu Ala Ala Val Ile Tyr Thr Asp Ala Leu Gln Thr				
	195		200	205
Leu Ile Met Leu Ile Gly Ala Leu Thr Leu Met Gly Tyr Ser Phe Ala				
	210		215	220
Ala Val Gly Gly Met Glu Gly Leu Lys Glu Lys Tyr Phe Leu Ala Leu				
	225		230	235
Ala Ser Asn Arg Ser Glu Asn Ser Ser Cys Gly Leu Pro Arg Glu Asp				
	245		250	255
Ala Phe His Ile Phe Arg Asp Pro Leu Thr Ser Asp Leu Pro Trp Pro				
	260		265	270
Gly Val Leu Phe Gly Met Ser Ile Pro Ser Leu Trp Tyr Trp Cys Thr				
	275		280	285
Asp Gln Val Ile Val Gln Arg Thr Leu Ala Ala Lys Asn Leu Ser His				
	290		295	300
Ala Lys Gly Gly Ala Leu Met Ala Ala Tyr Leu Lys Val Leu Pro Leu				
	305		310	315
Phe Ile Met Val Phe Pro Gly Met Val Ser Arg Ile Leu Phe Pro Asp				
	325		330	335
Gln Val Ala Cys Ala Asp Pro Glu Ile Cys Gln Lys Ile Cys Ser Asn				
	340		345	350

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Pro Ser Gly Cys Ser Asp Ile Ala Tyr Pro Lys Leu Val Leu Glu Leu
    355          360          365
Leu Pro Thr Gly Leu Arg Gly Leu Met Met Ala Val Met Val Ala Ala
    370          375          380
Leu Met Ser Ser Leu Thr Ser Ile Phe Asn Ser Ala Ser Thr Ile Phe
    385          390          395          400
Thr Met Asp Leu Trp Asn His Leu Arg Pro Arg Ala Ser Glu Lys Glu
    405          410          415
Leu Met Ile Val Gly Arg Val Phe Val Leu Leu Val Leu Val Ser
    420          425          430
Ile Leu Trp Ile Pro Val Val Gln Ala Ser Gln Gly Gly Gln Leu Phe
    435          440          445
Ile Tyr Ile Gln Ser Ile Ser Ser Tyr Leu Gln Pro Pro Val Ala Val
    450          455          460
Val Phe Ile Met Gly Cys Phe Trp Lys Arg Thr Asn Glu Lys Gly Ala
    465          470          475          480
Phe Trp Gly Leu Ile Ser Gly Leu Leu Leu Gly Leu Val Arg Leu Val
    485          490          495
Leu Asp Phe Ile Tyr Val Gln Pro Arg Cys Asp Gln Pro Asp Glu Arg
    500          505          510
Pro Val Leu Val Lys Ser Ile His Tyr Leu Tyr Phe Ser Met Ile Leu
    515          520          525
Ser Thr Val Thr Leu Ile Thr Val Ser Thr Val Ser Trp Phe Thr Glu
    530          535          540
Pro Pro Ser Lys Glu Met Val Ser His Leu Thr Trp Phe Thr Arg His
    545          550          555          560
Asp Pro Val Val Gln Lys Glu Gln Ala Pro Pro Ala Ala Pro Leu Ser
    565          570          575
Leu Thr Leu Ser Gln Asn Gly Met Pro Glu Ala Ser Ser Ser Ser Ser
    580          585          590
Val Gln Phe Glu Met Val Gln Glu Asn Thr Ser Lys Thr His Ser Cys
    595          600          605
Asp Met Thr Pro Lys Gln Ser Lys Val Val Lys Ala Ile Leu Trp Leu
    610          615          620
Cys Gly Ile Gln Glu Lys Gly Lys Glu Glu Leu Pro Ala Arg Ala Glu
    625          630          635          640
Ala Ile Ile Val Ser Leu Glu Glu Asn Pro Leu Val Lys Thr Leu Leu
    645          650          655
Asp Val Asn Leu Ile Phe Cys Val Ser Cys Ala Ile Phe Ile Trp Gly
    660          665          670
Tyr Phe Ala
    675

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<210> 76

<211> 485

<212> PRT

<213> homo sapiens

<400> 76

```

Met Glu Pro Cys Trp Gly Glu Gly Leu Phe His Leu Ala Pro Pro Arg
  1          5          10          15
His His Pro Gln Lys Ala Asp Trp His Phe Cys Pro Gln His Ile Gln
    20          25          30
Glu Phe Thr Asn Glu Thr Trp Gln Ala Arg Thr Gly Glu Pro Leu Pro
    35          40          45
Asp His Leu Val Leu Leu Met Trp Ser Leu Ile Val Ser Leu Tyr Pro
    50          55          60
Leu Gly Gly Leu Phe Gly Ala Leu Leu Ala Gly Pro Leu Ala Ile Thr

```

65					70					75				80
Leu	Gly	Arg	Lys	Lys	Ser	Leu	Leu	Val	Asn	Asn	Ile	Phe	Val	Ser
				85					90				95	
Ala	Ala	Ile	Leu	Phe	Gly	Phe	Ser	Arg	Lys	Ala	Gly	Ser	Phe	Glu
			100					105					110	Met
Ile	Met	Leu	Gly	Arg	Leu	Leu	Val	Gly	Val	Asn	Ala	Gly	Val	Ser
			115					120					125	Met
Asn	Ile	Gln	Pro	Met	Tyr	Leu	Gly	Glu	Ser	Ala	Pro	Lys	Glu	Leu
			130				135					140		Arg
Gly	Ala	Val	Ala	Met	Ser	Ser	Ala	Ile	Phe	Thr	Ala	Leu	Gly	Ile
145					150					155				160
Met	Gly	Gln	Val	Val	Gly	Leu	Arg	Glu	Leu	Leu	Gly	Gly	Pro	Gln
				165					170					175
Trp	Pro	Leu	Leu	Leu	Ala	Ser	Cys	Leu	Val	Pro	Gly	Ala	Leu	Gln
			180						185				190	Leu
Ala	Ser	Leu	Pro	Leu	Leu	Pro	Glu	Ser	Pro	Arg	Tyr	Leu	Leu	Ile
			195					200					205	Asp
Cys	Gly	Asp	Thr	Glu	Ala	Cys	Leu	Ala	Ala	Leu	Arg	Arg	Leu	Arg
210						215					220			Gly
Ser	Gly	Asp	Leu	Ala	Gly	Glu	Leu	Glu	Glu	Leu	Glu	Glu	Glu	Arg
225					230					235				240
Ala	Cys	Gln	Gly	Cys	Arg	Ala	Arg	Arg	Pro	Trp	Glu	Leu	Phe	Gln
				245					250					255
Arg	Ala	Leu	Arg	Arg	Gln	Val	Thr	Ser	Leu	Val	Val	Leu	Gly	Ser
			260					265					270	Ala
Met	Glu	Leu	Cys	Gly	Asn	Asp	Ser	Val	Tyr	Ala	Tyr	Ala	Ser	Ser
			275				280					285		Val
Phe	Arg	Lys	Ala	Gly	Val	Pro	Glu	Ala	Lys	Ile	Gln	Tyr	Ala	Ile
290						295					300			Ile
Gly	Thr	Gly	Ser	Cys	Glu	Leu	Leu	Thr	Ala	Val	Val	Ser	Cys	Val
305					310					315				320
Ile	Glu	Arg	Val	Gly	Arg	Arg	Val	Leu	Leu	Ile	Gly	Gly	Tyr	Ser
				325					330					335
Met	Thr	Cys	Trp	Gly	Ser	Ile	Phe	Thr	Val	Ala	Leu	Cys	Leu	Gln
			340					345					350	Ser
Ser	Phe	Pro	Trp	Thr	Leu	Tyr	Leu	Ala	Met	Ala	Cys	Ile	Phe	Ala
			355				360					365		Phe
Ile	Leu	Ser	Phe	Gly	Ile	Gly	Pro	Ala	Gly	Val	Thr	Gly	Ile	Leu
370						375					380			Ala
Thr	Glu	Leu	Phe	Asp	Gln	Met	Ala	Arg	Pro	Ala	Ala	Cys	Met	Val
385					390					395				Cys
Gly	Ala	Leu	Met	Trp	Ile	Met	Leu	Ile	Leu	Val	Gly	Leu	Gly	Phe
				405					410					415
Phe	Ile	Met	Glu	Ala	Leu	Ser	His	Phe	Leu	Tyr	Val	Pro	Phe	Leu
			420					425					430	Gly
Val	Cys	Val	Cys	Gly	Ala	Ile	Tyr	Thr	Gly	Leu	Phe	Leu	Pro	Glu
			435				440					445		Thr
Lys	Gly	Lys	Thr	Phe	Gln	Glu	Ile	Ser	Lys	Glu	Leu	His	Arg	Leu
			450			455					460			Asn
Phe	Pro	Arg	Arg	Ala	Gln	Gly	Pro	Thr	Trp	Arg	Ser	Leu	Glu	Val
465					470					475				480
Gln	Ser	Thr	Glu	Leu										
				485										

<210> 77

<211> 496

<212> PRT

<213> homo sapiens

<400> 77

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Met Arg Ala Leu Arg Arg Leu Ile Gln Gly Arg Ile Leu Leu Leu Thr
 1           5           10           15
Ile Cys Ala Ala Gly Ile Gly Gly Thr Phe Gln Phe Gly Tyr Asn Leu
      20           25           30
Ser Ile Ile Asn Ala Pro Thr Leu His Ile Gln Glu Phe Thr Asn Glu
      35           40           45
Thr Trp Gln Ala Arg Thr Gly Glu Pro Leu Pro Asp His Leu Val Leu
 50           55           60
Leu Met Trp Ser Leu Ile Val Ser Leu Tyr Pro Leu Gly Gly Leu Phe
65           70           75           80
Gly Ala Leu Leu Ala Gly Pro Leu Ala Ile Thr Leu Gly Arg Lys Lys
      85           90           95
Ser Leu Leu Val Asn Asn Ile Phe Val Val Ser Ala Ala Ile Leu Phe
      100           105           110
Gly Phe Ser Arg Lys Ala Gly Ser Phe Glu Met Ile Met Leu Gly Arg
      115           120           125
Leu Leu Val Gly Val Asn Ala Gly Val Ser Met Asn Ile Gln Pro Met
      130           135           140
Tyr Leu Gly Glu Ser Ala Pro Lys Glu Leu Arg Gly Ala Val Ala Met
145           150           155           160
Ser Ser Ala Ile Phe Thr Ala Leu Gly Ile Val Met Gly Gln Val Val
      165           170           175
Gly Leu Arg Glu Leu Leu Gly Gly Pro Gln Ala Trp Pro Leu Leu Leu
      180           185           190
Ala Ser Cys Leu Val Pro Gly Ala Leu Gln Leu Ala Ser Leu Pro Leu
      195           200           205
Leu Pro Glu Ser Pro Arg Tyr Leu Leu Ile Asp Cys Gly Asp Thr Glu
      210           215           220
Ala Cys Leu Ala Ala Leu Arg Arg Leu Arg Gly Ser Gly Asp Leu Ala
225           230           235           240
Gly Glu Leu Glu Glu Leu Glu Glu Glu Arg Ala Ala Cys Gln Gly Cys
      245           250           255
Arg Ala Arg Arg Pro Trp Glu Leu Phe Gln His Arg Ala Leu Arg Arg
      260           265           270
Gln Val Thr Ser Leu Val Val Leu Gly Ser Ala Met Glu Leu Cys Gly
      275           280           285
Asn Asp Ser Val Tyr Ala Tyr Ala Ser Ser Val Phe Arg Lys Ala Gly
      290           295           300
Val Pro Glu Ala Lys Ile Gln Tyr Ala Ile Ile Gly Thr Gly Ser Cys
305           310           315           320
Glu Leu Leu Thr Ala Val Val Ser Cys Val Val Ile Glu Arg Val Gly
      325           330           335
Arg Arg Val Leu Leu Ile Gly Gly Tyr Ser Leu Met Thr Cys Trp Gly
      340           345           350
Ser Ile Phe Thr Val Ala Leu Cys Leu Gln Ser Ser Phe Pro Trp Thr
      355           360           365
Leu Tyr Leu Ala Met Ala Cys Ile Phe Ala Phe Ile Leu Ser Phe Gly
      370           375           380
Ile Gly Pro Ala Gly Val Thr Gly Ile Leu Ala Thr Glu Leu Phe Asp
385           390           395           400
Gln Met Ala Arg Pro Ala Ala Cys Met Val Cys Gly Ala Leu Met Trp
      405           410           415
Ile Met Leu Ile Leu Val Gly Leu Gly Phe Pro Phe Ile Met Glu Ala
      420           425           430
Leu Ser His Phe Leu Tyr Val Pro Phe Leu Gly Val Cys Val Cys Gly
      435           440           445
Ala Ile Tyr Thr Gly Leu Phe Leu Pro Glu Thr Lys Gly Lys Thr Phe

```

450		455		460
Gln Glu Ile Ser Lys Glu Leu His Arg Leu Asn Phe Pro Arg Arg Ala				
465	470	475	480	
Gln Gly Pro Thr Trp Arg Ser Leu Glu Val Ile Gln Ser Thr Glu Leu				
485	490		495	

<210> 78

<211> 500

<212> PRT

<213> homo sapiens

<400> 78

Asx Met Leu His Ala Leu Leu Arg Ser Arg Met Ile Gln Gly Arg Ile				
1	5	10	15	
Leu Leu Leu Thr Ile Cys Ala Ala Gly Ile Gly Gly Thr Phe Gln Phe				
	20	25	30	
Gly Tyr Asn Leu Ser Ile Ile Asn Ala Pro Thr Leu His Ile Gln Glu				
	35	40	45	
Phe Thr Asn Glu Thr Trp Gln Ala Arg Thr Gly Glu Pro Leu Pro Asp				
	50	55	60	
His Leu Val Leu Leu Met Trp Ser Leu Ile Val Ser Leu Tyr Pro Leu				
65	70	75	80	
Gly Gly Leu Phe Gly Ala Leu Leu Ala Gly Pro Leu Ala Ile Thr Leu				
	85	90	95	
Gly Arg Lys Lys Ser Leu Leu Val Asn Asn Ile Phe Val Val Ser Ala				
	100	105	110	
Ala Ile Leu Phe Gly Phe Ser Arg Lys Ala Gly Ser Phe Glu Met Ile				
	115	120	125	
Met Leu Gly Arg Leu Leu Val Gly Val Asn Ala Gly Val Ser Met Asn				
	130	135	140	
Ile Gln Pro Met Tyr Leu Gly Glu Ser Ala Pro Lys Glu Leu Arg Gly				
145	150	155	160	
Ala Val Ala Met Ser Ser Ala Ile Phe Thr Ala Leu Gly Ile Val Met				
	165	170	175	
Gly Gln Val Val Gly Leu Arg Glu Leu Leu Gly Gly Pro Gln Ala Trp				
	180	185	190	
Pro Leu Leu Leu Ala Ser Cys Leu Val Pro Gly Ala Leu Gln Leu Ala				
	195	200	205	
Ser Leu Pro Leu Leu Pro Glu Ser Pro Arg Tyr Leu Leu Ile Asp Cys				
	210	215	220	
Gly Asp Thr Glu Ala Cys Leu Ala Ala Leu Arg Arg Leu Arg Gly Ser				
225	230	235	240	
Gly Asp Leu Ala Gly Glu Leu Glu Glu Leu Glu Glu Arg Ala Ala				
	245	250	255	
Cys Gln Gly Cys Arg Ala Arg Arg Pro Trp Glu Leu Phe Gln His Arg				
	260	265	270	
Ala Leu Arg Arg Gln Val Thr Ser Leu Val Val Leu Gly Ser Ala Met				
	275	280	285	
Glu Leu Cys Gly Asn Asp Ser Val Tyr Ala Tyr Ala Ser Ser Val Phe				
	290	295	300	
Arg Lys Ala Gly Val Pro Glu Ala Lys Ile Gln Tyr Ala Ile Ile Gly				
305	310	315	320	
Thr Gly Ser Cys Glu Leu Leu Thr Ala Val Val Ser Cys Val Val Ile				
	325	330	335	
Glu Arg Val Gly Arg Arg Val Leu Leu Ile Gly Gly Tyr Ser Leu Met				
	340	345	350	
Thr Cys Trp Gly Ser Ile Phe Thr Val Ala Leu Cys Leu Gln Ser Ser				
	355	360	365	

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Phe Pro Trp Thr Leu Tyr Leu Ala Met Ala Cys Ile Phe Ala Phe Ile
 370          375          380
Leu Ser Phe Gly Ile Gly Pro Ala Gly Val Thr Gly Ile Leu Ala Thr
385          390          395          400
Glu Leu Phe Asp Gln Met Ala Arg Pro Ala Ala Cys Met Val Cys Gly
          405          410          415
Ala Leu Met Trp Ile Met Leu Ile Leu Val Gly Leu Gly Phe Pro Phe
          420          425          430
Ile Met Glu Ala Leu Ser His Phe Leu Tyr Val Pro Phe Leu Gly Val
          435          440          445
Cys Val Cys Gly Ala Ile Tyr Thr Gly Leu Phe Leu Pro Glu Thr Lys
          450          455          460
Gly Lys Thr Phe Gln Glu Ile Ser Lys Glu Leu His Arg Leu Asn Phe
465          470          475          480
Pro Arg Arg Ala Gln Gly Pro Thr Trp Arg Ser Leu Glu Val Ile Gln
          485          490          495
Ser Thr Glu Leu
          500

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<210> 79
<211> 1358
<212> PRT
<213> homo sapiens

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<400> 79
Met Val Val Val Lys Pro Met Asn Thr Met Ala Pro Val Val Thr Arg
 1          5          10          15
Asn Thr Gly Leu Ile Leu Tyr Glu Gly Gln Ser Arg Pro Leu Thr Gly
          20          25          30
Pro Ala Gly Ser Gly Pro Gln Asn Leu Val Ile Ser Asp Glu Asp Asp
          35          40          45
Leu Glu Ala Val Arg Leu Glu Val Val Ala Gly Leu Arg His Gly His
          50          55          60
Leu Val Ile Leu Gly Ala Ser Ser Gly Ser Ser Ala Pro Lys Ser Phe
65          70          75          80
Thr Val Ala Glu Leu Ala Ala Gly Gln Val Val Tyr Gln His Asp Asp
          85          90          95
Arg Asp Gly Ser Leu Ser Asp Asn Leu Val Leu Arg Met Val Asp Gly
          100          105          110
Gly Gly Arg His Gln Val Gln Phe Leu Phe Pro Ile Thr Leu Val Pro
          115          120          125
Val Asp Asp Gln Pro Pro Val Leu Asn Ala Asn Thr Gly Leu Thr Leu
          130          135          140
Ala Glu Gly Glu Thr Val Pro Ile Leu Pro Leu Ser Leu Ser Ala Thr
145          150          155          160
Asp Met Asp Ser Asp Asp Ser Leu Leu Leu Phe Val Leu Glu Ser Pro
          165          170          175
Phe Leu Thr Thr Gly His Leu Leu Leu Arg Gln Thr His Pro Pro His
          180          185          190
Glu Lys Gln Glu Leu Leu Arg Gly Leu Trp Arg Lys Glu Gly Ala Phe
          195          200          205
Tyr Glu Arg Thr Val Thr Glu Trp Gln Gln Gln Asp Ile Thr Glu Gly
          210          215          220
Arg Leu Phe Tyr Arg His Ser Gly Pro His Ser Pro Gly Pro Val Thr
225          230          235          240
Asp Gln Phe Thr Phe Arg Val Gln Asp Asn His Asp Pro Pro Asn Gln
          245          250          255
Ser Gly Leu Gln Arg Phe Val Ile Arg Ile His Pro Val Asp Arg Leu

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Pro	Pro	Glu	Leu	Gly	Ser	Gly	Cys	Pro	Leu	Arg	Met	Val	Val	Gln	Glu
		275					280					285			
Ser	Gln	Leu	Thr	Pro	Leu	Arg	Lys	Lys	Trp	Leu	Arg	Tyr	Thr	Asp	Leu
		290				295					300				
Asp	Thr	Asp	Asp	Arg	Glu	Leu	Arg	Tyr	Thr	Val	Thr	Gln	Ser	Pro	Thr
305				310						315				320	
Asp	Thr	Asp	Glu	Asn	His	Leu	Pro	Ala	Pro	Leu	Gly	Thr	Leu	Val	Leu
				325					330					335	
Thr	Asp	Asn	Pro	Ser	Val	Val	Val	Thr	His	Phe	Thr	Gln	Ala	Gln	Ile
			340					345					350		
Asn	His	His	Lys	Ile	Ala	Tyr	Arg	Pro	Pro	Gly	Gln	Glu	Leu	Gly	Val
		355					360					365			
Ala	Thr	Arg	Val	Ala	Gln	Phe	Gln	Phe	Gln	Val	Glu	Asp	Arg	Ala	Gly
		370				375					380				
Asn	Val	Ala	Pro	Gly	Thr	Phe	Thr	Leu	Tyr	Leu	His	Pro	Val	Asp	Asn
385					390					395				400	
Gln	Pro	Pro	Glu	Ile	Leu	Asn	Thr	Gly	Phe	Thr	Ile	Gln	Glu	Lys	Gly
			405					410						415	
His	His	Ile	Leu	Ser	Glu	Thr	Glu	Leu	His	Val	Asn	Asp	Val	Asp	Thr
			420					425					430		
Asp	Val	Ala	His	Ile	Ser	Phe	Thr	Leu	Thr	Gln	Ala	Pro	Lys	His	Gly
		435					440					445			
His	Met	Arg	Val	Ser	Gly	Gln	Ile	Leu	His	Val	Gly	Gly	Leu	Phe	His
		450				455				460					
Leu	Glu	Asp	Ile	Lys	Gln	Gly	Arg	Val	Ser	Tyr	Ala	His	Asn	Gly	Asp
465				470						475				480	
Lys	Ser	Leu	Thr	Asp	Ser	Cys	Ser	Leu	Glu	Val	Ser	Asp	Arg	His	His
				485					490					495	
Val	Val	Pro	Ile	Thr	Leu	Arg	Val	Asn	Val	Arg	Pro	Val	Asp	Asp	Glu
			500					505					510		
Val	Pro	Ile	Leu	Ser	His	Pro	Thr	Gly	Thr	Leu	Glu	Ser	Tyr	Leu	Asp
		515					520					525			
Val	Leu	Glu	Asn	Gly	Ala	Thr	Glu	Ile	Thr	Ala	Asn	Val	Ile	Lys	Gly
		530				535					540				
Thr	Asn	Glu	Glu	Thr	Asp	Asp	Leu	Met	Leu	Thr	Phe	Leu	Leu	Glu	Asp
545					550					555				560	
Pro	Pro	Leu	Tyr	Gly	Glu	Ile	Leu	Val	Asn	Gly	Ile	Pro	Ala	Glu	Gln
				565					570					575	
Phe	Thr	Gln	Arg	Asp	Ile	Leu	Glu	Gly	Ser	Val	Val	Tyr	Thr	His	Thr
			580					585					590		
Ser	Gly	Glu	Ile	Gly	Leu	Leu	Pro	Lys	Ala	Asp	Ser	Phe	Asn	Leu	Ser
		595					600					605			
Leu	Ser	Asp	Met	Ser	Gln	Glu	Trp	Arg	Ile	Gly	Gly	Asn	Thr	Ile	Gln
		610				615					620				
Gly	Val	Thr	Ile	Trp	Val	Thr	Ile	Leu	Pro	Val	Asp	Ser	Gln	Ala	Pro
625					630					635				640	
Glu	Ile	Phe	Val	Gly	Glu	Gln	Leu	Ile	Val	Met	Glu	Gly	Asp	Lys	Ser
				645					650					655	
Val	Ile	Thr	Ser	Val	His	Ile	Ser	Ala	Glu	Asp	Val	Asp	Ser	Leu	Asn
			660					665				670			
Asp	Asp	Ile	Leu	Cys	Thr	Ile	Val	Ile	Gln	Pro	Thr	Ser	Gly	Tyr	Val
		675					680					685			
Glu	Asn	Ile	Ser	Pro	Ala	Pro	Gly	Ser	Glu	Lys	Ser	Arg	Ala	Gly	Ile
		690				695					700				
Ala	Ile	Ser	Ala	Phe	Asn	Leu	Lys	Asp	Leu	Arg	Gln	Gly	His	Ile	Asn
705					710					715				720	
Tyr	Val	Gln	Ser	Val	His	Lys	Gly	Val	Glu	Pro	Val	Glu	Asp	Arg	Phe
				725					730					735	

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Val Phe Arg Cys Ser Asp Gly Ile Asn Phe Ser Glu Arg Gln Phe Phe
      740      745      750
Pro Ile Val Ile Ile Pro Thr Asn Asp Glu Gln Pro Glu Met Phe Met
      755      760      765
Arg Glu Phe Met Val Met Glu Gly Met Ser Leu Val Ile Asp Thr Pro
      770      775      780
Ile Leu Asn Ala Ala Asp Ala Asp Val Pro Leu Asp Asp Leu Thr Phe
      785      790      795      800
Thr Ile Thr Gln Phe Pro Thr His Gly His Ile Met Asn Gln Leu Ile
      805      810      815
Asn Gly Thr Val Leu Val Glu Ser Phe Thr Leu Asp Gln Ile Ile Glu
      820      825      830
Ser Ser Ser Ile Ile Tyr Glu His Asp Asp Ser Glu Thr Gln Glu Asp
      835      840      845
Ser Phe Val Ile Lys Leu Thr Asp Gly Lys His Ser Val Glu Lys Thr
      850      855      860
Val Leu Ile Ile Val Ile Pro Val Asp Asp Glu Thr Pro Arg Met Thr
      865      870      875      880
Ile Asn Asn Gly Leu Glu Ile Glu Ile Gly Asp Thr Lys Ile Ile Asn
      885      890      895
Asn Lys Ile Leu Met Ala Thr Asp Leu Asp Ser Glu Asp Lys Ser Leu
      900      905      910
Val Tyr Ile Ile Arg Tyr Gly Pro Gly His Gly Leu Leu Gln Arg Arg
      915      920      925
Lys Pro Thr Gly Ala Phe Glu Asn Ile Thr Leu Gly Met Asn Phe Thr
      930      935      940
Gln Asp Glu Val Asp Arg Asn Leu Ile Gln Tyr Val His Leu Gly Gln
      945      950      955      960
Glu Gly Ile Arg Asp Leu Ile Lys Phe Asp Val Thr Asp Gly Ile Asn
      965      970      975
Pro Leu Ile Asp Arg Tyr Phe Tyr Val Ser Ile Gly Ser Ile Asp Ile
      980      985      990
Val Phe Pro Asp Val Ile Ser Lys Gly Val Ser Leu Lys Glu Gly Gly
      995      1000      1005
Lys Val Thr Leu Thr Thr Asp Leu Leu Ser Thr Ser Asp Leu Asn Ser
      1010      1015      1020
Pro Asp Glu Asn Leu Val Phe Thr Ile Thr Arg Ala Pro Met Arg Gly
      1025      1030      1035      1040
His Leu Glu Cys Thr Asp Gln Pro Gly Val Ser Ile Thr Ser Phe Thr
      1045      1050      1055
Gln Leu Gln Leu Ala Gly Asn Lys Ile Tyr Tyr Ile His Thr Ala Asp
      1060      1065      1070
Asp Glu Val Lys Met Asp Ser Phe Glu Phe Gln Val Thr Asp Gly Arg
      1075      1080      1085
Asn Pro Val Phe Arg Thr Phe Arg Ile Ser Ile Ser Asp Val Asp Asn
      1090      1095      1100
Lys Lys Pro Val Val Thr Ile His Lys Leu Val Val Ser Glu Ser Glu
      1105      1110      1115      1120
Asn Lys Leu Ile Thr Pro Phe Glu Leu Thr Val Glu Asp Arg Asp Thr
      1125      1130      1135
Pro Asp Lys Leu Leu Lys Phe Thr Ile Thr Gln Val Pro Ile His Gly
      1140      1145      1150
His Leu Leu Phe Asn Asn Thr Arg Pro Val Met Val Phe Thr Lys Gln
      1155      1160      1165
Asp Leu Asn Glu Asn Leu Ile Ser Tyr Lys His Asp Gly Thr Glu Ser
      1170      1175      1180
Ser Glu Asp Ser Phe Ser Phe Thr Val Thr Asp Gly Thr His Thr Asp
      1185      1190      1195      1200
Phe Tyr Val Phe Pro Asp Thr Val Phe Glu Thr Arg Arg Pro Gln Val

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      1205      1210      1215
Met Lys Ile Gln Val Leu Ala Val Asp Asn Ser Val Pro Gln Ile Ala
      1220      1225      1230
Val Asn Lys Gly Ala Ser Thr Leu Arg Thr Leu Ala Thr Gly His Leu
      1235      1240      1245
Gly Phe Met Ile Thr Ser Lys Ile Leu Lys Val Glu Asp Arg Asp Ser
      1250      1255      1260
Leu His Ile Ser Leu Arg Phe Ile Val Thr Glu Ala Pro Gln His Gly
      1265      1270      1275      1280
Tyr Leu Leu Asn Leu Asp Lys Gly Asn His Ser Ile Thr Gln Phe Thr
      1285      1290      1295
Gln Ala Asp Ile Asp Asp Met Lys Ile Cys Tyr Val Leu Arg Glu Gly
      1300      1305      1310
Ala Asn Ala Thr Ser Asp Met Phe Tyr Phe Ala Val Glu Asp Gly Gly
      1315      1320      1325
Lys Tyr Ser Pro Leu Leu Val Val Thr Ala Arg Arg Asp Ala Phe Leu
      1330      1335      1340
Gly Cys Ser Leu Met Thr Leu Leu Gln Glu Val Phe Ile Lys
      1345      1350      1355

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<210> 80

<211> 3105

<212> PRT

<213> homo sapiens

<400> 80

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Met Ala Arg Ser Trp Leu Thr Ala Thr Ser Thr Ser Arg Pro Ala Ala
 1      5      10      15
Phe Gly Arg Ala Leu Leu Ser Pro Gly Leu Ala Gly Ala Ala Gly Val
      20      25      30
Pro Ala Glu Ala Ile Val Leu Ala Asn Arg Gly Leu Arg Val Pro
      35      40      45
Phe Gly Arg Glu Val Trp Leu Asp Pro Leu His Asp Leu Val Leu Gln
      50      55      60
Val Gln Pro Gly Asp Arg Cys Ala Val Ser Val Leu Asp Asn Asp Ala
      65      70      75      80
Leu Ala Gln Arg Pro Gly Arg Leu Ser Pro Lys Arg Phe Pro Cys Asp
      85      90      95
Phe Gly Pro Gly Glu Val Arg Tyr Ser His Leu Gly Ala Arg Ser Pro
      100      105      110
Ser Arg Asp Arg Val Arg Leu Gln Leu Arg Tyr Asp Ala Pro Gly Gly
      115      120      125
Ala Val Val Leu Pro Leu Val Leu Glu Val Glu Val Phe Thr Gln
      130      135      140
Leu Glu Val Val Thr Arg Asn Leu Pro Leu Val Val Glu Glu Leu Leu
      145      150      155      160
Gly Thr Ser Asn Ala Leu Asp Ala Arg Ser Leu Glu Phe Ala Phe Gln
      165      170      175
Pro Glu Thr Glu Glu Cys Arg Val Gly Ile Leu Ser Gly Leu Gly Ala
      180      185      190
Leu Pro Arg Tyr Gly Glu Leu Leu His Tyr Pro Gln Val Pro Gly Gly
      195      200      205
Ala Arg Glu Gly Gly Ala Pro Glu Thr Leu Leu Met Asp Cys Lys Ala
      210      215      220
Phe Gln Glu Leu Gly Val Arg Tyr Arg His Thr Ala Ala Ser Arg Ser
      225      230      235      240
Pro Asn Arg Asp Trp Ile Pro Met Val Val Glu Leu Arg Ser Arg Gly
      245      250      255

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Ala Pro Val Gly Ser Pro Ala Leu Lys Arg Glu His Phe Gln Val Leu
 260 265 270
 Val Arg Ile Arg Gly Gly Ala Glu Asn Thr Ala Pro Lys Pro Ser Phe
 275 280 285
 Val Ala Met Met Met Met Glu Val Asp Gln Phe Val Leu Thr Ala Leu
 290 295 300
 Thr Pro Asp Met Leu Ala Ala Glu Asp Ala Glu Ser Pro Ser Asp Leu
 305 310 315 320
 Leu Ile Phe Asn Leu Thr Ser Pro Phe Gln Pro Gly Gln Gly Tyr Leu
 325 330 335
 Val Ser Thr Asp Asp Arg Ser Leu Pro Leu Ser Ser Phe Thr Gln Arg
 340 345 350
 Asp Leu Arg Leu Leu Lys Ile Ala Tyr Gln Pro Pro Ser Glu Asp Ser
 355 360 365
 Asp Gln Glu Arg Leu Phe Glu Leu Glu Leu Glu Val Val Asp Leu Glu
 370 375 380
 Gly Ala Ala Ser Asp Pro Phe Ala Phe Met Val Val Val Lys Pro Met
 385 390 395 400
 Asn Thr Met Ala Pro Val Val Thr Arg Asn Thr Gly Leu Ile Leu Tyr
 405 410 415
 Glu Gly Gln Ser Arg Pro Leu Thr Gly Pro Ala Gly Ser Gly Pro Gln
 420 425 430
 Asn Leu Val Ile Ser Asp Glu Asp Asp Leu Glu Ala Val Arg Leu Glu
 435 440 445
 Val Val Ala Gly Leu Arg His Gly His Leu Val Ile Leu Gly Ala Ser
 450 455 460
 Ser Gly Ser Ser Ala Pro Lys Ser Phe Thr Val Ala Glu Leu Ala Ala
 465 470 475 480
 Gly Gln Val Val Tyr Gln His Asp Asp Arg Asp Gly Ser Leu Ser Asp
 485 490 495
 Asn Leu Val Leu Arg Met Val Asp Gly Gly Arg His Gln Val Gln
 500 505 510
 Phe Leu Phe Pro Ile Thr Leu Val Pro Val Asp Asp Gln Pro Pro Val
 515 520 525
 Leu Asn Ala Asn Thr Gly Leu Thr Leu Ala Glu Gly Glu Thr Val Pro
 530 535 540
 Ile Leu Pro Leu Ser Leu Ser Ala Thr Asp Met Asp Ser Asp Asp Ser
 545 550 555 560
 Leu Leu Leu Phe Val Leu Glu Ser Pro Phe Leu Thr Thr Gly His Leu
 565 570 575
 Leu Leu Arg Gln Thr His Pro Pro His Glu Lys Gln Glu Leu Leu Arg
 580 585 590
 Gly Leu Trp Arg Lys Glu Gly Ala Phe Tyr Glu Arg Thr Val Thr Glu
 595 600 605
 Trp Gln Gln Gln Asp Ile Thr Glu Gly Arg Leu Phe Tyr Arg His Ser
 610 615 620
 Gly Pro His Ser Pro Gly Pro Val Thr Asp Gln Phe Thr Phe Arg Val
 625 630 635 640
 Gln Asp Asn His Asp Pro Pro Asn Gln Ser Gly Leu Gln Arg Phe Val
 645 650 655
 Ile Arg Ile His Pro Val Asp Arg Leu Pro Pro Glu Leu Gly Ser Gly
 660 665 670
 Cys Pro Leu Arg Met Val Val Gln Glu Ser Gln Leu Thr Pro Leu Arg
 675 680 685
 Lys Lys Trp Leu Arg Tyr Thr Asp Leu Asp Thr Asp Asp Arg Glu Leu
 690 695 700
 Arg Tyr Thr Val Thr Gln Pro Pro Thr Asp Thr Asp Glu Asn His Leu
 705 710 715 720
 Pro Ala Pro Leu Gly Thr Leu Val Leu Thr Asp Asn Pro Ser Val Val

64/79

His Gly His Ile Met Asn Gln Leu Ile Asn Gly Thr Val Leu Val Glu
 1205 1210 1215
 Ser Phe Thr Leu Asp Gln Ile Ile Glu Ser Ser Ser Ile Ile Tyr Glu
 1220 1225 1230
 His Asp Asp Ser Glu Thr Gln Glu Asp Ser Phe Val Ile Lys Leu Thr
 1235 1240 1245
 Asp Gly Lys His Ser Val Glu Lys Thr Val Leu Ile Ile Val Ile Pro
 1250 1255 1260
 Val Asp Asp Glu Thr Pro Arg Met Thr Ile Asn Asn Gly Leu Glu Ile
 1265 1270 1275 1280
 Glu Ile Gly Asp Thr Lys Ile Ile Asn Asn Lys Ile Leu Met Ala Thr
 1285 1290 1295
 Asp Leu Asp Ser Glu Asp Lys Ser Leu Val Tyr Ile Ile Arg Tyr Gly
 1300 1305 1310
 Pro Gly His Gly Leu Leu Gln Arg Arg Lys Pro Thr Gly Ala Phe Glu
 1315 1320 1325
 Asn Ile Thr Leu Gly Met Asn Phe Thr Gln Asp Glu Val Asp Arg Asn
 1330 1335 1340
 Leu Ile Gln Tyr Val His Leu Gly Gln Glu Gly Ile Arg Asp Leu Ile
 1345 1350 1355 1360
 Lys Phe Asp Val Thr Asp Gly Ile Asn Pro Leu Ile Asp Arg Tyr Phe
 1365 1370 1375
 Tyr Val Ser Ile Gly Ser Ile Asp Ile Val Phe Pro Asp Val Ile Ser
 1380 1385 1390
 Lys Gly Val Ser Leu Lys Glu Gly Lys Val Thr Leu Thr Thr Asp
 1395 1400 1405
 Leu Leu Ser Thr Ser Asp Leu Asn Ser Pro Asp Glu Asn Leu Val Phe
 1410 1415 1420
 Thr Ile Thr Arg Ala Pro Met Arg Gly His Leu Glu Cys Thr Asp Gln
 1425 1430 1435 1440
 Pro Gly Val Ser Ile Thr Ser Phe Thr Gln Leu Gln Leu Ala Gly Asn
 1445 1450 1455
 Lys Ile Tyr Tyr Ile His Thr Ala Asp Asp Glu Val Lys Met Asp Ser
 1460 1465 1470
 Phe Glu Phe Gln Val Thr Asp Gly Arg Asn Pro Val Phe Arg Thr Phe
 1475 1480 1485
 Arg Ile Ser Ile Ser Asp Val Asp Asn Lys Lys Pro Val Val Thr Ile
 1490 1495 1500
 His Lys Leu Val Val Ser Glu Ser Glu Asn Lys Leu Ile Thr Pro Phe
 1505 1510 1515 1520
 Glu Leu Thr Val Glu Asp Arg Asp Thr Pro Asp Lys Leu Leu Lys Phe
 1525 1530 1535
 Thr Ile Thr Gln Val Pro Ile His Gly His Leu Leu Phe Asn Asn Thr
 1540 1545 1550
 Arg Pro Val Met Val Phe Thr Lys Gln Asp Leu Asn Glu Asn Leu Ile
 1555 1560 1565
 Ser Tyr Lys His Asp Gly Thr Glu Ser Ser Glu Asp Ser Phe Ser Phe
 1570 1575 1580
 Thr Val Thr Asp Gly Thr His Thr Asp Phe Tyr Val Phe Pro Asp Thr
 1585 1590 1595 1600
 Val Phe Glu Thr Arg Arg Pro Gln Val Met Lys Ile Gln Val Leu Ala
 1605 1610 1615
 Val Asp Asn Ser Val Pro Gln Ile Ala Val Asn Lys Gly Ala Ser Thr
 1620 1625 1630
 Leu Arg Thr Leu Ala Thr Gly His Leu Gly Phe Met Ile Thr Ser Lys
 1635 1640 1645
 Ile Leu Lys Val Glu Asp Arg Asp Ser Leu His Ile Ser Leu Arg Phe
 1650 1655 1660
 Ile Val Thr Glu Ala Pro Gln His Gly Tyr Leu Leu Asn Leu Asp Lys

1665		1670		1675		1680
Gly Asn His Ser Ile Thr Gln Phe Thr Gln Ala Asp Ile Asp Asp Met						
	1685			1690		1695
Lys Ile Cys Tyr Val Leu Arg Glu Gly Ala Asn Ala Thr Ser Asp Met						
	1700		1705			1710
Phe Tyr Phe Ala Val Glu Asp Gly Gly Gly Asn Lys Leu Thr Tyr Gln						
	1715		1720			1725
Asn Phe Arg Leu Asn Trp Ala Trp Ile Ser Phe Glu Lys Glu Tyr Tyr						
	1730		1735			1740
Leu Val Asn Glu Asp Ser Lys Phe Leu Asp Val Val Leu Lys Arg Arg						
	1745		1750			1755
Gly Tyr Leu Gly Glu Thr Ser Phe Ile Ser Ile Gly Thr Arg Asp Arg						
	1765		1770			1775
Thr Ala Glu Lys Asp Lys Asp Phe Lys Gly Lys Ala Gln Lys Gln Val						
	1780		1785			1790
Gln Phe Asn Pro Gly Gln Thr Arg Ala Thr Trp Arg Val Arg Ile Leu						
	1795		1800			1805
Ser Asp Gly Glu His Glu Gln Ser Glu Thr Phe Gln Val Val Leu Ser						
	1810		1815			1820
Glu Pro Val Leu Ala Ala Leu Glu Phe Pro Thr Val Ala Thr Val Glu						
	1825		1830			1835
Ile Val Asp Pro Gly Asp Glu Pro Thr Val Phe Ile Pro Gln Ser Lys						
	1845		1850			1855
Tyr Ser Val Glu Glu Asp Val Gly Glu Leu Phe Ile Pro Ile Arg Arg						
	1860		1865			1870
Ser Gly Asp Val Ser Gln Glu Leu Met Val Val Cys Tyr Thr Gln Gln						
	1875		1880			1885
Gly Thr Ala Thr Gly Thr Val Pro Thr Ser Val Leu Ser Tyr Ser Asp						
	1890		1895			1900
Tyr Ile Ser Arg Pro Glu Asp His Thr Ser Val Val Arg Phe Asp Lys						
	1905		1910			1915
Asp Glu Arg Glu Lys Leu Cys Arg Ile Val Ile Ile Asp Asp Ser Leu						
	1925		1930			1935
Tyr Glu Glu Glu Glu Thr Phe His Val Leu Leu Ser Met Pro Met Gly						
	1940		1945			1950
Gly Arg Ile Gly Ser Glu Phe Pro Gly Ala Gln Val Thr Ile Val Pro						
	1955		1960			1965
Asp Lys Asp Asp Gly Pro Ser Asp Ser Lys Phe Asn Val Ala Glu Asn						
	1970		1975			1980
Tyr Ser Leu Leu Pro Phe Thr Cys Phe Gln Gly Ser Ile Ala Thr Ala						
	1985		1990			1995
Glu Ala Ala Thr Gln Gly Gly Gly Arg Ser Thr Arg Gln Val Ala Ala						
	2005		2010			2015
Val Lys Lys Asp Lys Asp Phe Lys Gly Lys Ala Gln Lys Gln Val Gln						
	2020		2025			2030
Phe Asn Pro Gly Gln Thr Arg Ala Thr Trp Arg Val Arg Ile Leu Ser						
	2035		2040			2045
Asp Gly Glu His Glu Gln Ser Glu Thr Phe Gln Val Val Leu Ser Glu						
	2050		2055			2060
Pro Val Leu Ala Ala Leu Glu Phe Pro Thr Val Ala Thr Val Glu Ile						
	2065		2070			2075
Val Asp Pro Gly Asp Ala Cys Pro Trp Gly Glu Glu Ser Asp Gln Ser						
	2085		2090			2095
Ser Gln Gly Leu Lys Leu Gln Ser Phe Leu Thr Lys Met Met Val Ser						
	2100		2105			2110
Thr Asn Leu Leu Glu Asn Ser Phe Ser Arg Glu Asp Gln His Gln Glu						
	2115		2120			2125
Gln Leu Ser Arg Gln Lys Lys Trp Glu Ser Lys Thr Met Ile Ile Tyr						
	2130		2135			2140

Thr Phe Ile Leu Cys Glu Thr Glu Lys Pro Cys Ile Leu Glu Leu Met
 2145 2150 2155 2160
 Asp Asp Val Leu Tyr Glu Glu Val Glu Glu Leu Arg Leu Val Leu Gly
 2165 2170 2175
 Thr Pro Gln Ser Asn Ser Pro Phe Gly Ala Ala Val Gly Glu Gln Asn
 2180 2185 2190
 Glu Thr Leu Ile Arg Ile Arg Asp Asp Ala Asp Lys Thr Val Ile Lys
 2195 2200 2205
 Phe Gly Glu Thr Lys Phe Ser Val Thr Glu Pro Lys Glu Pro Gly Glu
 2210 2215 2220
 Ser Val Val Ile Arg Ile Pro Val Ile Arg Gln Gly Asp Thr Ser Lys
 2225 2230 2235 2240
 Val Ser Ile Val Arg Val His Thr Lys Asp Gly Ser Ala Thr Ser Gly
 2245 2250 2255
 Glu Asp Tyr His Pro Val Ser Glu Glu Ile Glu Phe Lys Glu Gly Glu
 2260 2265 2270
 Thr Gln His Val Val Glu Ile Glu Val Thr Phe Asp Gly Val Arg Glu
 2275 2280 2285
 Met Arg Glu Ala Phe Thr Val His Leu Lys Pro Asp Glu Asn Met Ile
 2290 2295 2300
 Ala Glu Met Gln Leu Ser Asn Phe Glu Leu Thr Leu Ser Pro Asp Gly
 2305 2310 2315 2320
 Thr Arg Val Gly Asn His Lys Cys Ser Asn Leu Leu Asp Tyr Thr Glu
 2325 2330 2335
 Val Lys Thr His Tyr Gly Phe Leu Thr Asp Ala Thr Lys Asn Pro Glu
 2340 2345 2350
 Ile Ile Gly Glu Thr Tyr Pro Tyr Gln Tyr Ser Leu Ser Ile Arg Gly
 2355 2360 2365
 Ser Thr Thr Leu Arg Phe Tyr Arg Asn Leu Asn Leu Glu Ala Cys Leu
 2370 2375 2380
 Trp Glu Phe Val Ser Tyr Tyr Asp Met Ser Glu Leu Leu Ala Asp Cys
 2385 2390 2395 2400
 Arg Ser Val Leu Asn Ala Ser Ile Phe His Glu Met Ala Pro Glu Gly
 2405 2410 2415
 Lys Gln Ser Lys Cys Leu Val Asn Ser Thr Leu Tyr Ser Ile Leu Glu
 2420 2425 2430
 Cys His Glu Ser Leu Pro Asn Phe Cys Ile Ser Ala Leu Arg Met Gly
 2435 2440 2445
 Lys Trp Arg Lys Ile Lys Ser Lys Pro Ser Ala Gln Thr Pro Cys Ala
 2450 2455 2460
 Gln Arg Leu Arg Gly Phe Ile Asp His Pro Arg Lys Gln Pro Leu Gln
 2465 2470 2475 2480
 Gln Ala Ser Ala Asp Pro Gly Met Leu Pro Val Ile Ser Thr Arg Glu
 2485 2490 2495
 Leu Ser Asn Phe Glu Leu Thr Leu Ser Pro Asp Gly Thr Arg Val Gly
 2500 2505 2510
 Asn His Lys Cys Ser Asn Leu Leu Asp Tyr Thr Glu Val Lys Thr His
 2515 2520 2525
 Tyr Gly Phe Leu Thr Asp Ala Thr Lys Asn Pro Glu Ile Ile Gly Glu
 2530 2535 2540
 Thr Tyr Pro Tyr Gln Tyr Ser Leu Ser Ile Arg Gly Ser Thr Thr Leu
 2545 2550 2555 2560
 Arg Phe Tyr Arg Asn Leu Asn Leu Glu Ala Cys Leu Trp Glu Phe Val
 2565 2570 2575
 Ser Tyr Tyr Asp Met Ser Glu Leu Leu Ala Asp Cys Gly Gly Thr Ile
 2580 2585 2590
 Gly Thr Asp Gly Gln Val Leu Asn Leu Val Gln Ser Tyr Val Thr Leu
 2595 2600 2605
 Arg Val Pro Leu Tyr Val Ser Tyr Val Phe His Ser Pro Val Gly Val

2610	2615	2620
Gly Gly Trp Gln His Phe Asp Leu Lys Ser Glu Leu Arg Leu Thr Phe		
2625	2630	2635
Val Tyr Asp Thr Ala Ile Leu Trp Asn Asp Gly Ile Gly Ser Pro Pro		
	2645	2650
Glu Ala Glu Leu Gln Gly Ser Leu Tyr Pro Thr Ser Met Arg Ile Gly		2655
	2660	2665
Asp Glu Gly Arg Leu Ala Val His Phe Lys Thr Glu Ala Gln Phe His		2670
	2675	2680
Gly Leu Phe Val Leu Ser His Pro Ala Ser Phe Thr Ser Ser Val Ile		2685
	2690	2700
Met Ser Ala Asp His Pro Gly Leu Thr Phe Ser Leu Arg Leu Ile Arg		
2705	2710	2715
Ser Glu Pro Thr Tyr Asn Gln Pro Val Gln Gln Trp Ser Phe Val Ser		2720
	2725	2730
Asp Phe Ala Val Arg Asp Tyr Ser Gly Thr Tyr Thr Val Lys Leu Val		2735
	2740	2745
Pro Cys Thr Ala Pro Ser His Gln Glu Tyr Arg Leu Pro Val Thr Cys		2750
	2755	2760
Asn Pro Arg Glu Pro Val Thr Phe Asp Leu Asp Ile Arg Phe Gln Gln		2765
	2770	2775
Val Ser Asp Pro Val Ala Ala Glu Phe Ser Leu Asn Thr Gln Met Tyr		2780
2785	2790	2795
Leu Leu Ser Lys Lys Ser Leu Trp Leu Ser Asp Gly Ser Met Gly Phe		2800
	2805	2810
Gly Gln Glu Ser Asp Val Ala Phe Ala Glu Gly Asp Ile Ile Tyr Gly		2815
	2820	2825
Arg Val Met Val Asp Pro Val Gln Asn Leu Gly Asp Ser Phe Tyr Cys		2830
	2835	2840
Ser Ile Glu Lys Val Phe Leu Cys Thr Gly Ala Asp Gly Tyr Val Pro		2845
	2850	2855
Lys Tyr Ser Pro Met Asn Ala Glu Tyr Gly Cys Leu Ala Asp Ser Pro		2860
2865	2870	2875
Ser Leu Leu Tyr Arg Phe Lys Ile Val Asp Lys Ala Gln Pro Glu Thr		2880
	2885	2890
Gln Ala Thr Ser Phe Gly Asn Val Leu Phe Asn Ala Lys Leu Ala Val		2895
	2900	2905
Asp Asp Pro Glu Ala Ile Leu Leu Val Asn Gln Pro Gly Ser Asp Gly		2910
	2915	2920
Phe Lys Val Asp Ser Thr Pro Leu Phe Gln Val Ala Leu Gly Arg Glu		2925
	2930	2935
Trp Tyr Ile His Thr Ile Tyr Thr Val Arg Ser Lys Asp Asn Ala Asn		2940
2945	2950	2955
Arg Gly Ile Gly Lys Arg Ser Val Glu Tyr His Ser Leu Val Ser Gln		2960
	2965	2970
Gly Lys Pro Gln Ser Thr Thr Lys Ser Arg Lys Lys Arg Glu Ile Arg		2975
	2980	2985
Ser Thr Pro Ser Leu Ala Trp Glu Ile Gly Ala Glu Asn Ser Arg Gly		2990
	2995	3000
Thr Asn Ile Gln His Ile Ala Leu Asp Arg Thr Lys Arg Gln Ile Pro		3005
	3010	3015
His Gly Arg Ala Pro Pro Asp Gly Ile Leu Pro Trp Glu Leu Asn Ser		3020
3025	3030	3035
Pro Ser Ser Ala Val Ser Leu Val Thr Val Val Gly Gly Thr Thr Val		3040
	3045	3050
Gly Leu Leu Thr Ile Cys Leu Thr Val Ile Ala Val Leu Met Cys Arg		3055
	3060	3065
Gly Lys Glu Ser Phe Arg Gly Lys Asp Ala Pro Lys Gly Ser Ser Ser		3070
	3075	3080
		3085

Ser Glu Pro Met Val Pro Pro Gln Ser His His Asn Asp Ser Ser Glu
 3090 3095 3100
 Val
 3105

<210> 81
 <211> 457
 <212> PRT
 <213> homo sapiens

<400> 81
 Met Gly Cys Ser Gly Ala Trp Gly Leu Ser Cys Pro Cys Pro Gln Thr
 1 5 10 15
 Pro Ser Trp Ala Trp Arg Lys Met Arg Thr Pro Ser Met Arg Asn Arg
 20 25 30
 Ser Gly Ala Val Trp Ser Arg Ala Ser Val Pro Phe Ser Ala Trp Glu
 35 40 45
 Val Glu Val Gln Met Arg Val Thr Gly Leu Gly Arg Arg Gly Ala Gln
 50 55 60
 Gly Met Ala Val Trp Tyr Thr Arg Gly Arg Gly His Val Gly Ser Val
 65 70 75 80
 Leu Gly Gly Leu Ala Ser Trp Asp Gly Ile Gly Ile Phe Phe Asp Ser
 85 90 95
 Pro Ala Glu Asp Thr Gln Asp Ser Pro Ala Ile Arg Val Leu Ala Ser
 100 105 110
 Asp Gly His Ile Pro Ser Glu Gln Pro Gly Asp Gly Ala Ser Gln Gly
 115 120 125
 Leu Gly Ser Cys His Trp Asp Phe Arg Asn Arg Pro His Pro Phe Arg
 130 135 140
 Ala Arg Ile Thr Tyr Trp Gly Gln Arg Leu Arg Met Ser Leu Asn Ser
 145 150 155 160
 Gly Leu Thr Pro Ser Asp Pro Gly Glu Phe Cys Val Asp Val Gly Pro
 165 170 175
 Leu Leu Leu Val Pro Gly Gly Phe Phe Gly Val Ser Ala Ala Thr Gly
 180 185 190
 Thr Leu Ala Asp Asp His Asp Val Leu Ser Phe Leu Thr Phe Ser Leu
 195 200 205
 Ser Glu Pro Ser Pro Glu Val Pro Pro Gln Pro Phe Leu Glu Met Gln
 210 215 220
 His Val Arg Leu Ala Arg Gln Leu Glu Gly Leu Trp Ala Arg Leu Gly
 225 230 235 240
 Leu Gly Thr Arg Glu Asp Val Thr Pro Lys Ser Asp Ser Glu Ala Gln
 245 250 255
 Gly Glu Gly Glu Arg Leu Phe Asp Leu Glu Glu Thr Leu Gly Arg His
 260 265 270
 Arg Arg Ile Leu Gln Ala Leu Arg Gly Leu Ser Lys Gln Leu Ala Gln
 275 280 285
 Ala Glu Arg Gln Trp Lys Lys Gln Leu Gly Pro Gln Ala Lys Pro Gly
 290 295 300
 Leu Thr Glu Ala Gly Asp Ala Ala Val Arg Met Ala Ala Glu Ala Gln
 305 310 315 320
 Val Ser Tyr Leu Pro Val Gly Ile Glu His His Phe Leu Glu Leu Asp
 325 330 335
 His Ile Leu Gly Leu Leu Gln Glu Glu Leu Arg Gly Pro Ala Lys Ala
 340 345 350
 Ala Ala Lys Ala Pro Arg Pro Pro Gly Gln Pro Pro Arg Ala Ser Ser
 355 360 365
 Cys Leu Gln Pro Gly Ile Phe Leu Phe Tyr Leu Leu Ile Gln Thr Val

370		375		380
Gly Phe Phe Gly Tyr Val His Phe Arg Arg Pro Val Pro Arg Pro Ala				
385		390		395
Lys Thr Met Ala Phe Met Val Lys Thr Met Val Gly Gly Gln Leu Lys				400
	405		410	415
Asn Leu Thr Gly Ser Leu Gly Gly Gly Glu Asp Lys Gly Asp Gly Asp				
	420		425	430
Lys Ser Ala Ala Glu Ala Gln Gly Met Ser Arg Glu Glu Tyr Glu Glu				
	435		440	445
Tyr Gln Lys Gln Leu Val Glu Glu Lys				
450		455		

<210> 82

<211> 526

<212> PRT

<213> homo sapiens

<400> 82

Met Pro Ala Val Ser Gly Pro Gly Pro Leu Phe Cys Leu Leu Leu Leu				
1	5	10	15	
Leu Leu Asp Pro His Ser Pro Glu Thr Gly Cys Pro Pro Leu Arg Arg				
	20	25	30	
Phe Glu Tyr Lys Leu Ser Phe Lys Gly Pro Arg Leu Ala Leu Pro Gly				
	35	40	45	
Ala Gly Ile Pro Phe Trp Ser His His Gly Asp Ala Ile Leu Gly Leu				
	50	55	60	
Glu Glu Val Arg Leu Thr Pro Ser Met Arg Asn Arg Ser Gly Ala Val				
	65	70	75	80
Trp Ser Arg Ala Ser Val Pro Phe Ser Ala Trp Glu Val Glu Val Gln				
	85	90	95	
Met Arg Val Thr Gly Leu Gly Arg Arg Gly Ala Gln Gly Met Ala Val				
	100	105	110	
Trp Tyr Thr Arg Gly Arg Gly His Val Gly Ser Val Leu Gly Gly Leu				
	115	120	125	
Ala Ser Trp Asp Gly Ile Gly Ile Phe Phe Asp Ser Pro Ala Glu Asp				
	130	135	140	
Thr Gln Asp Ser Pro Ala Ile Arg Val Leu Ala Ser Asp Gly His Ile				
	145	150	155	160
Pro Ser Glu Gln Pro Gly Asp Gly Ala Ser Gln Gly Leu Gly Ser Cys				
	165	170	175	
His Trp Asp Phe Arg Asn Arg Pro His Pro Phe Arg Ala Arg Ile Thr				
	180	185	190	
Tyr Trp Gly Gln Arg Leu Arg Met Ser Leu Asn Ser Gly Leu Thr Pro				
	195	200	205	
Ser Asp Pro Gly Glu Phe Cys Val Asp Val Gly Pro Leu Leu Leu Val				
	210	215	220	
Pro Gly Gly Phe Phe Gly Val Ser Ala Ala Thr Gly Thr Leu Ala Asp				
	225	230	235	240
Asp His Asp Val Leu Ser Phe Leu Thr Phe Ser Leu Ser Glu Pro Ser				
	245	250	255	
Pro Glu Val Pro Pro Gln Pro Phe Leu Glu Met Gln His Val Arg Leu				
	260	265	270	
Ala Arg Gln Leu Glu Gly Leu Trp Ala Arg Leu Gly Leu Gly Thr Arg				
	275	280	285	
Glu Asp Val Thr Pro Lys Ser Asp Ser Glu Ala Gln Gly Glu Gly Glu				
	290	295	300	
Arg Leu Phe Asp Leu Glu Glu Thr Leu Gly Arg His Arg Arg Ile Leu				
	305	310	315	320

Gln Ala Leu Arg Gly Leu Ser Lys Gln Leu Ala Gln Ala Glu Arg Gln
 325 330 335
 Trp Lys Lys Gln Leu Gly Pro Pro Gly Gln Ala Arg Pro Asp Gly Gly
 340 345 350
 Trp Ala Leu Asp Ala Ser Cys Gln Ile Pro Ser Thr Pro Gly Arg Gly
 355 360 365
 Gly His Leu Ser Met Ser Leu Asn Lys Asp Ser Ala Lys Val Gly Ala
 370 375 380
 Leu Leu His Gly Gln Trp Thr Leu Leu Gln Ala Leu Gln Glu Met Arg
 385 390 395 400
 Asp Ala Ala Val Arg Met Ala Ala Glu Ala Gln Val Ser Tyr Leu Pro
 405 410 415
 Val Gly Ile Glu His His Phe Leu Glu Leu Asp His Ile Leu Gly Leu
 420 425 430
 Leu Gln Glu Glu Leu Arg Gly Pro Ala Lys Ala Ala Lys Ala Pro
 435 440 445
 Arg Pro Pro Gly Gln Pro Pro Arg Ala Ser Ser Cys Leu Gln Pro Gly
 450 455 460
 Ile Phe Leu Phe Tyr Leu Leu Ile Gln Thr Val Gly Phe Phe Gly Tyr
 465 470 475 480
 Val His Phe Arg Gln Glu Leu Asn Lys Ser Leu Gln Glu Cys Leu Ser
 485 490 495
 Thr Gly Ser Leu Pro Leu Gly Pro Ala Pro His Thr Pro Arg Ala Leu
 500 505 510
 Gly Ile Leu Arg Arg Gln Pro Leu Pro Ala Ser Met Pro Ala
 515 520 525

<210> 83

<211> 904

<212> PRT

<213> homo sapiens

<400> 83

Met Leu Leu Ala Leu Cys Ser Ser Leu Ala Leu Ile Phe Ala Ala Pro
 1 5 10 15
 Val Ser Gly Gln Leu Glu His Ser Gly Asn Tyr Tyr Cys Thr Ala Asp
 20 25 30
 Asn Gly Phe Gly Pro Gln His Ser Glu Val Val Ser Leu Ser Val Thr
 35 40 45
 Val Pro Val Ser His Pro Val Leu Thr Leu Ser Ser Ala Glu Ala Leu
 50 55 60
 Thr Phe Glu Gly Ala Thr Val Thr Leu His Ser Ser Leu Ile Leu Gln
 65 70 75 80
 Ala Pro Leu Ser Val Phe Glu Gly Asp Phe Val Val Leu Arg Cys Arg
 85 90 95
 Ala Lys Ala Glu Val Thr Leu Asn Thr Met Tyr Lys Asn Gly Asn Val
 100 105 110
 Leu Thr Phe Leu Asn Lys Ser Ser Asp Phe His Ile His His Ala Ser
 115 120 125
 Leu Lys Asp Asn Gly Ala Tyr His Phe Thr Gly Phe Asn Gly Ser Asn
 130 135 140
 Phe Ser Val Ser Ser Asn Ile Val Lys Ile Gln Val Gln Glu His Leu
 145 150 155 160
 Leu Pro Gln Trp Phe Leu Lys Ala Pro Asp Pro Thr Val Ala Leu Ser
 165 170 175
 Glu Ile Phe Ser Val Asn Arg Gly Pro Leu Leu Thr Gly Thr Gly Ser
 180 185 190
 Arg Val Met Thr Pro Trp Ile Tyr Phe Pro Thr Glu Asp Trp Asn Phe

	195						200						205					
Thr 210	Leu	Ile	Pro	Ile	Thr	Val	Asp	Asp	Ala	Cys	Lys	Arg	Pro	Cys	Ala			
Pro 225	Arg	Ala	Pro	Trp	Glu	Val	Gly	Ser	Leu	Thr	Pro	Gly	Lys	Ser	Phe			
Gln 240	Gln	Lys	Gly	Asn	Pro	Asp	Leu	Leu	Met	Gly	Pro	Phe	Asp	Val	Leu			
His	Leu	Ser	Leu	Ile	Thr	Leu	Phe	Cys	Asn	Met	Ala	Gly	Ser	Leu	Phe			
Tyr	Tyr	Met	Glu	Leu	Gly	Glu	Lys	Lys	Asp	Ala	Leu	Phe	Val	Thr	Gly			
Asn 290	Glu	Ser	Arg	Ser	Tyr	His	Trp	Phe	Gln	Lys	Phe	Ser	Leu	Ala	Gly			
Gly 305	Gln	Glu	Ala	Asp	Gln	Lys	Leu	Trp	Phe	Pro	Pro	Gly	Leu	Met	Ser			
Gln	Asp	Ile	Phe	Ile	Tyr	Ile	Arg	Gln	Gly	Glu	Ser	Cys	Leu	Val	Ile			
Glu	Met	Phe	His	Gln	Val	Tyr	Arg	Arg	Pro	Ala	Gly	Gly	Val	Pro	Val			
Glu	His	Met	Ser	Val	Trp	Ala	Leu	Arg	Val	Asn	Ser	Ser	Gly	Leu	Phe			
Ala 370	Tyr	Ala	Asp	Gly	Trp	Leu	Phe	Thr	Leu	Phe	Gln	Leu	Gln	Ser	Val			
Asp 385	Asn	Leu	Ser	Pro	Ser	Thr	Gln	Ser	Gln	Thr	His	Glu	Gly	His	Glu			
Lys	Leu	Cys	Pro	Phe	Leu	Ala	Ile	Gly	Pro	Pro	Ala	His	Ser	Arg	Gly			
Ser	Phe	Leu	Arg	Ala	Lys	Lys	Ser	Leu	Val	Ala	Tyr	Ile	Lys	Gly	Asn			
Gln	Leu	Ser	Phe	Pro	Pro	Val	Glu	Asp	Leu	Leu	Pro	Lys	Ser	Gln	Trp			
Pro 450	Cys	Ile	Gln	Val	Leu	Pro	Arg	Asn	Ile	Ala	Ala	Ala	Ala	His	Lys			
Pro 465	Val	Ile	Ser	Val	His	Pro	Pro	Trp	Thr	Thr	Phe	Phe	Lys	Gly	Glu			
Arg	Val	Thr	Leu	Thr	Cys	Asn	Gly	Phe	Gln	Phe	Tyr	Ala	Thr	Glu	Lys			
Thr	Thr	Trp	Tyr	His	Arg	His	Tyr	Trp	Gly	Glu	Lys	Leu	Thr	Leu	Thr			
Pro	Gly	Asn	Thr	Leu	Glu	Val	Arg	Glu	Ser	Gly	Leu	Tyr	Arg	Cys	Gln			
Ala 530	Arg	Gly	Ser	Pro	Arg	Ser	Asn	Pro	Val	Arg	Leu	Leu	Phe	Ser	Ser			
Gly 545	Glu	Lys	Glu	Asp	Cys	Val	Ser	Asp	Lys	Asn	Pro	Ala	Thr	Asn	His			
Thr	Pro	Met	Ser	Arg	Lys	Arg	Ser	Ser	Cys	Ser	Ser	Leu	Ser	Ala	Thr			
Ser	Phe	Ile	Ala	Pro	Ala	Leu	Arg	Leu	Asp	Ser	Leu	Ile	Leu	Gln	Ala			
Pro	Tyr	Ser	Val	Phe	Glu	Gly	Asp	Thr	Leu	Val	Leu	Arg	Cys	His	Arg			
Arg	Arg	Lys	Glu	Lys	Leu	Thr	Ala	Val	Lys	Tyr	Thr	Trp	Asn	Gly	Asn			
Ile 625	Leu	Ser	Ile	Ser	Asn	Lys	Ser	Trp	Asp	Leu	Leu	Ile	Pro	Gln	Ala			
Ser	Ser	Asn	Asn	Asn	Gly	Asn	Tyr	Arg	Cys	Ile	Gly	Tyr	Gly	Asp	Glu			
Asn	Asp	Val	Phe	Arg	Ser	Asn	Phe	Lys	Ile	Ile	Lys	Ile	Gln	Gly	Ile			

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Pro Val Ser Gly Val Leu Leu Glu Thr Gln Pro Ser Gly Gly Gln Ala
675 680 685
Val Glu Gly Glu Met Leu Val Leu Val Cys Ser Val Ala Glu Gly Thr
690 695 700
Gly Asp Thr Thr Phe Ser Trp His Arg Glu Asp Met Gln Glu Ser Leu
705 710 715 720
Gly Arg Lys Thr Gln Arg Ser Leu Arg Ala Glu Leu Glu Leu Pro Ala
725 730 735
Ile Arg Gln Ser His Ala Gly Gly Tyr Tyr Cys Thr Ala Asp Asn Ser
740 745 750
Tyr Gly Pro Val Gln Ser Met Val Leu Asn Val Thr Val Arg Glu Thr
755 760 765
Pro Gly Asn Arg Asp Gly Leu Val Ala Ala Gly Ala Thr Gly Gly Leu
770 775 780
Leu Ser Ala Leu Leu Leu Ala Val Ala Leu Leu Phe His Cys Trp Arg
785 790 795 800
Arg Arg Lys Ser Val His Pro Lys Lys Gly Asp Leu Val Tyr Ser Glu
805 810 815
Ile Gln Thr Thr Gln Leu Gly Glu Glu Glu Gly Asn His Gly Asn
820 825 830
Lys Asn Gln Glu Leu Glu Leu Val Asn Val Gly Glu Ser Phe Ser His
835 840 845
Arg Ala Cys Ile Trp Ser Thr Leu Met Gly Thr Cys Gln Thr Ile Gly
850 855 860
Gly Ala Asn Thr Ser Arg Thr Leu Leu Glu Asp Lys Asp Val Ser Val
865 870 875 880
Val Tyr Ser Glu Val Lys Thr Gln His Pro Asp Asn Ser Ala Gly Lys
885 890 895
Ile Ser Ser Lys Asp Glu Glu Ser
900

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<210> 84

<211> 515

<212> PRT

<213> homo sapiens

<400> 84

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Met Leu Leu Trp Ala Ser Leu Leu Ala Phe Ala Pro Val Cys Gly Gln
1 5 10 15
Ser Ala Ala Ala His Lys Pro Val Ile Ser Val His Pro Pro Trp Thr
20 25 30
Thr Phe Phe Lys Gly Glu Arg Val Thr Leu Thr Cys Asn Gly Phe Gln
35 40 45
Phe Tyr Ala Thr Glu Lys Thr Trp Tyr His Arg His Tyr Trp Gly
50 55 60
Glu Lys Leu Thr Leu Thr Pro Gly Asn Thr Leu Glu Val Arg Glu Ser
65 70 75 80
Gly Leu Tyr Arg Cys Gln Ala Arg Gly Ser Pro Arg Ser Asn Pro Val
85 90 95
Arg Leu Leu Phe Ser Ser Asp Ser Leu Ile Leu Gln Ala Pro Tyr Ser
100 105 110
Val Phe Glu Gly Asp Thr Leu Val Leu Arg Cys His Arg Arg Lys
115 120 125
Glu Lys Leu Thr Ala Val Lys Tyr Thr Trp Asn Gly Asn Ile Leu Ser
130 135 140
Ile Ser Asn Lys Ser Trp Asp Leu Leu Ile Pro Gln Ala Ser Ser Asn
145 150 155 160
Asn Asn Gly Asn Tyr Arg Cys Ile Gly Tyr Gly Asp Glu Asn Asp Val

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      165      170      175
Phe Arg Ser Asn Phe Lys Ile Ile Lys Ile Gln Glu Leu Phe Pro His
      180      185      190
Pro Glu Leu Lys Ala Thr Asp Ser Gln Pro Thr Glu Gly Asn Ser Val
      195      200      205
Asn Leu Ser Cys Glu Thr Gln Leu Pro Pro Glu Arg Ser Asp Thr Pro
      210      215      220
Leu His Phe Asn Phe Phe Arg Asp Gly Glu Val Ile Leu Ser Asp Trp
      225      230      235
Ser Thr Tyr Pro Glu Leu Gln Leu Pro Thr Val Trp Arg Glu Asn Ser
      245      250      255
Gly Ser Tyr Trp Cys Gly Ala Glu Thr Val Arg Gly Asn Ile His Lys
      260      265      270
His Ser Pro Ser Leu Gln Ile His Val Gln Arg Ile Pro Val Ser Gly
      275      280      285
Val Leu Leu Glu Thr Gln Pro Ser Gly Gly Gln Ala Val Glu Gly Glu
      290      295      300
Met Leu Val Leu Val Cys Ser Val Ala Glu Gly Thr Gly Asp Thr Thr
      305      310      315
Phe Ser Trp His Arg Glu Asp Met Gln Glu Ser Leu Gly Arg Lys Thr
      325      330      335
Gln Arg Ser Leu Arg Ala Glu Leu Glu Leu Pro Ala Ile Arg Gln Ser
      340      345      350
His Ala Gly Gly Tyr Tyr Cys Thr Ala Asp Asn Ser Tyr Gly Pro Val
      355      360      365
Gln Ser Met Val Leu Asn Val Thr Val Arg Glu Thr Pro Gly Asn Arg
      370      375      380
Asp Gly Leu Val Ala Ala Gly Ala Thr Gly Gly Leu Leu Ser Ala Leu
      385      390      395
Leu Leu Ala Val Ala Leu Leu Phe His Cys Trp Arg Arg Arg Lys Ser
      405      410      415
Gly Val Gly Phe Leu Gly Asp Glu Thr Arg Leu Pro Pro Ala Pro Gly
      420      425      430
Pro Gly Glu Ser Ser His Ser Ile Cys Pro Ala Gln Val Glu Leu Gln
      435      440      445
Ser Leu Tyr Val Asp Val His Pro Lys Lys Gly Asp Leu Val Tyr Ser
      450      455      460
Glu Ile Gln Thr Thr Gln Leu Gly Glu Glu Glu Ala Asn Thr Ser
      465      470      475
Arg Thr Leu Leu Glu Asp Lys Asp Val Ser Val Val Tyr Ser Glu Val
      485      490      495
Lys Thr Gln His Pro Asp Asn Ser Ala Gly Lys Ile Ser Ser Lys Asp
      500      505      510
Glu Glu Ser
      515

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<210> 85

<211> 831

<212> PRT

<213> homo sapiens

<400> 85

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Asx Met Ala Val Gly Gly Gly His Lys Gly Val Arg Cys Pro Pro Ser
  1          5          10          15
Ala Arg Ser Ser Gln Val Pro Thr Cys Cys Ala Gly Trp Arg Gln Gln
      20      25      30
Gly Asp Glu Cys Gly Ile Ala Val Cys Glu Gly Asn Ser Thr Cys Ser
      35      40      45

```

Glu Asn Glu Val Cys Val Arg Pro Gly Glu Cys Arg Cys Arg His Gly
 50 55 60
 Tyr Phe Gly Ala Asn Cys Asp Thr Lys Cys Pro Arg Gln Phe Trp Gly
 65 70 75 80
 Pro Asp Cys Lys Glu Leu Cys Ser Cys His Pro His Gly Gln Cys Glu
 85 90 95
 Asp Val Thr Gly Gln Cys Thr Cys His Ala Arg Arg Trp Gly Ala Arg
 100 105 110
 Cys Glu His Ala Cys Gln Cys Gln His Gly Thr Cys His Pro Arg Ser
 115 120 125
 Gly Ala Cys Arg Cys Glu Ser Gly Trp Trp Gly Ala Gln Cys Ala Ser
 130 135 140
 Ala Cys Tyr Cys Ser Ala Thr Ser Arg Cys Asp Pro Gln Thr Gly Ala
 145 150 155 160
 Cys Leu Cys His Ala Gly Trp Trp Gly Arg Ser Cys Asn Asn Gln Cys
 165 170 175
 Ala Cys Asn Ser Ser Pro Cys Glu Gln Gln Ser Gly Arg Cys Gln Cys
 180 185 190
 Arg Glu Arg Thr Phe Gly Ala Arg Cys Asp Arg Tyr Cys Gln Cys Phe
 195 200 205
 Arg Gly Arg Cys His Pro Val Asp Gly Thr Cys Ala Cys Glu Pro Gly
 210 215 220
 Tyr Arg Gly Lys Tyr Cys Arg Glu Pro Cys Pro Ala Gly Phe Tyr Gly
 225 230 235 240
 Leu Gly Cys Arg Arg Arg Cys Gly Gln Cys Lys Gly Gln Gln Pro Cys
 245 250 255
 Thr Val Ala Glu Gly Arg Cys Leu Thr Cys Glu Pro Gly Trp Asn Gly
 260 265 270
 Thr Lys Cys Asp Gln Pro Cys Ala Thr Gly Phe Tyr Gly Glu Gly Cys
 275 280 285
 Ser His Arg Cys Pro Pro Cys Arg Asp Gly His Ala Cys Asn His Val
 290 295 300
 Thr Gly Lys Cys Thr Arg Cys Asn Ala Gly Trp Ile Gly Asp Arg Cys
 305 310 315 320
 Glu Thr Lys Cys Ser Asn Gly Thr Tyr Gly Glu Asp Cys Ala Phe Val
 325 330 335
 Cys Ala Asp Cys Gly Ser Gly His Cys Asp Phe Gln Ser Gly Arg Cys
 340 345 350
 Leu Cys Ser Pro Gly Val His Gly Pro His Cys Asn Val Thr Cys Pro
 355 360 365
 Pro Gly Leu His Gly Ala Asp Cys Ala Gln Ala Cys Ser Cys His Glu
 370 375 380
 Asp Thr Cys Asp Pro Val Thr Gly Ala Cys His Leu Glu Thr Asn Gln
 385 390 395 400
 Arg Lys Gly Val Met Gly Ala Gly Ala Leu Leu Val Leu Leu Val Cys
 405 410 415
 Leu Leu Leu Ser Leu Leu Gly Cys Cys Cys Ala Cys Arg Gly Lys Asp
 420 425 430
 Pro Thr Arg Arg Pro Arg Pro Arg Arg Glu Leu Ser Leu Gly Arg Lys
 435 440 445
 Lys Ala Pro His Arg Leu Cys Gly Arg Phe Ser Arg Ile Ser Met Lys
 450 455 460
 Leu Pro Arg Ile Pro Leu Arg Arg Gln Lys Leu Pro Lys Val Val Val
 465 470 475 480
 Ala His His Asp Leu Asp Asn Thr Leu Asn Cys Ser Phe Leu Glu Pro
 485 490 495
 Pro Ser Gly Leu Glu Gln Pro Ser Pro Ser Trp Ser Ser Arg Ala Ser
 500 505 510
 Phe Ser Ser Phe Asp Thr Thr Asp Glu Gly Pro Val Tyr Cys Val Pro

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      515      520      525
His Glu Glu Ala Pro Ala Glu Ser Arg Asp Pro Glu Val Pro Thr Val
530      535      540
Pro Ala Glu Ala Pro Ala Pro Ser Pro Val Pro Leu Thr Thr Pro Ala
545      550      555      560
Ser Ala Glu Glu Ala Ile Pro Leu Pro Ala Ser Ser Asp Ser Glu Arg
565      570      575
Ser Ala Ser Ser Val Glu Gly Pro Gly Gly Ala Leu Tyr Ala Arg Val
580      585      590
Ala Arg Arg Glu Ala Arg Pro Ala Arg Ala Arg Gly Glu Ile Gly Gly
595      600      605
Leu Ser Leu Ser Pro Ser Pro Glu Arg Arg Lys Pro Pro Pro Pro Asp
610      615      620
Pro Ala Thr Lys Pro Lys Val Ser Trp Ile His Gly Lys His Ser Ala
625      630      635      640
Ala Ala Ala Gly Arg Ala Pro Ser Pro Pro Pro Gly Ser Glu Ala
645      650      655
Ala Pro Ser Pro Ser Lys Arg Lys Arg Thr Pro Ser Asp Lys Ser Ala
660      665      670
His Thr Val Glu His Gly Ser Pro Arg Thr Arg Asp Pro Thr Pro Arg
675      680      685
Pro Pro Gly Leu Pro Glu Glu Ala Thr Ala Leu Ala Ala Pro Ser Pro
690      695      700
Pro Arg Ala Arg Ala Arg Ala Ala Pro Arg Pro Leu Gly Ala His Gly
705      710      715      720
Arg Arg Arg Ser Pro Ala Lys Arg Ala Glu Ala Ala Ser Met Leu Ala
725      730      735
Ala Asp Val Arg Gly Lys Thr Arg Ser Leu Gly Arg Ala Glu Val Ala
740      745      750
Leu Gly Ala Gln Gly Pro Arg Glu Lys Pro Ala Pro Pro Gln Lys Ala
755      760      765
Lys Arg Ser Val Pro Pro Ala Ser Pro Ala Arg Ala Pro Pro Ala Thr
770      775      780
Glu Thr Pro Gly Pro Glu Lys Ala Ala Thr Asp Leu Pro Ala Pro Glu
785      790      795      800
Thr Pro Arg Lys Lys Thr Pro Ile Gln Lys Pro Pro Arg Lys Lys Ser
805      810      815
Arg Glu Ala Ala Gly Glu Leu Gly Arg Ala Gly Ala Pro Thr Leu
820      825      830

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<210> 86

<211> 871

<212> PRT

<213> homo sapiens

<400> 86

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Asx Met Glu Gly Ala Gly Pro Arg Gly Ala Gly Pro Ala Arg Arg Arg
1      5      10      15
Gly Ala Gly Gly Pro Pro Ser Pro Leu Leu Pro Ser Leu Leu Leu Leu
20      25      30
Leu Leu Leu Trp Met Leu Pro Asp Thr Val Ala Pro Gln Glu Leu Asn
35      40      45
Pro Arg Gly Arg Asn Val Cys Arg Ala Pro Gly Ser Gln Val Pro Thr
50      55      60
Cys Cys Ala Gly Trp Arg Gln Gln Gly Asp Glu Cys Gly Ile Ala Val
65      70      75      80
Cys Glu Gly Asn Ser Thr Cys Ser Glu Asn Glu Val Cys Val Arg Pro
85      90      95

```

Gly Glu Cys Arg Cys Arg His Gly Tyr Phe Gly Ala Asn Cys Asp Thr
 100 105 110
 Lys Cys Pro Arg Gln Phe Trp Gly Pro Asp Cys Lys Glu Leu Cys Ser
 115 120 125
 Cys His Pro His Gly Gln Cys Glu Asp Val Thr Gly Gln Cys Thr Cys
 130 135 140
 His Ala Arg Arg Trp Gly Ala Arg Cys Glu His Ala Cys Gln Cys Gln
 145 150 155 160
 His Gly Thr Cys His Pro Arg Ser Gly Ala Cys Arg Cys Glu Ser Gly
 165 170 175
 Trp Trp Gly Ala Gln Cys Ala Ser Ala Cys Tyr Cys Ser Ala Thr Ser
 180 185 190
 Arg Cys Asp Pro Gln Thr Gly Ala Cys Leu Cys His Ala Gly Trp Trp
 195 200 205
 Gly Arg Ser Cys Asn Asn Gln Cys Ala Cys Asn Ser Ser Pro Cys Glu
 210 215 220
 Gln Gln Ser Gly Arg Cys Gln Cys Arg Glu Arg Thr Phe Gly Ala Arg
 225 230 235 240
 Cys Asp Arg Tyr Cys Gln Cys Phe Arg Gly Arg Cys His Pro Val Asp
 245 250 255
 Gly Thr Cys Ala Cys Glu Pro Gly Tyr Arg Gly Lys Tyr Cys Arg Glu
 260 265 270
 Pro Cys Pro Ala Gly Phe Tyr Gly Leu Gly Cys Arg Arg Arg Cys Gly
 275 280 285
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 325 330 335
 Asp Gly His Ala Cys Asn His Val Thr Gly Lys Cys Thr Arg Cys Asn
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 Ala Gly Trp Ile Gly Asp Arg Cys Glu Thr Lys Cys Ser Asn Gly Thr
 355 360 365
 Tyr Gly Glu Asp Cys Ala Phe Val Cys Ala Asp Cys Gly Ser Gly His
 370 375 380
 Cys Asp Phe Gln Ser Gly Arg Cys Leu Cys Ser Pro Gly Val His Gly
 385 390 395 400
 Pro His Cys Asn Val Thr Cys Pro Pro Gly Leu His Gly Ala Asp Cys
 405 410 415
 Ala Gln Ala Cys Ser Cys His Glu Asp Thr Cys Asp Pro Val Thr Gly
 420 425 430
 Ala Cys His Leu Glu Thr Asn Gln Arg Lys Gly Val Met Gly Ala Gly
 435 440 445
 Ala Leu Leu Val Leu Leu Val Cys Leu Leu Leu Ser Leu Leu Gly Cys
 450 455 460
 Cys Cys Ala Cys Arg Gly Lys Asp Pro Thr Arg Arg Pro Arg Pro Arg
 465 470 475 480
 Arg Glu Leu Ser Leu Gly Arg Lys Lys Ala Pro His Arg Leu Cys Gly
 485 490 495
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			20					25					30		
Glu	Gln	Gly	Ala	Ala	Val	Asn	Leu	Arg	Asp	Glu	Arg	Gly	Arg	Thr	Ala
		35					40					45			
Leu	Ser	Leu	Ala	Cys	Glu	Arg	Gly	His	Leu	Asp	Ala	Val	Gln	Leu	Leu
	50					55					60				
Val	Gln	Phe	Ser	Gly	Asp	Pro	Glu	Ala	Ala	Asp	Ser	Ala	Gly	Asn	Ser
65				70						75				80	
Pro	Val	Met	Trp	Ala	Ala	Ala	Cys	Gly	His	Gly	Ala	Val	Leu	Glu	Phe
				85					90					95	

Leu Val Arg Ser Phe Arg Arg Leu Gly Leu Arg Leu Asp Arg Thr Asn
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 Thr Cys Val Gln Ala Leu
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<210> 88

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<212> PRT

<213> homo sapiens

<400> 88

Met Leu Lys Pro Lys Asp Leu Cys Pro Arg Ala Gly Thr Arg Thr Phe
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 20 25 30
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 35 40 45
 Thr Pro Leu Met Val Ala Val Gly Leu Pro Asp Pro Ala Leu Arg Ala
 50 55 60
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 65 70 75 80
 Asp Glu Arg Gly Arg Thr Ala Leu Ser Leu Ala Cys Glu Arg Gly His
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 Leu Asp Ala Val Gln Leu Leu Val Gln Phe Ser Gly Asp Pro Glu Ala
 100 105 110
 Ala Asp Ser Ala Gly Asn Ser Pro Val Met Trp Ala Ala Ala Cys Gly
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 His Gly Ala Val Leu Glu Phe Leu Val Arg Ser Phe Arg Arg Leu Gly
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 145 150 155 160
 Ala Ala Ala Arg Gly His Gly Thr Ser Ala Gly Gly His Gly Gly Glu
 165 170 175
 Ala Gly Ser Ala Gly Lys Asn Ser Gly Arg His Arg Ala Gln Gly Ser
 180 185 190
 Glu Arg Pro Glu Leu Gly Arg Ser Met Ser Leu Ala Leu Gly Ala Val
 195 200 205
 Thr Glu Glu Glu Ala Ala Arg Leu Arg Ala Gly Ala Leu Met Ala Leu
 210 215 220
 Pro Asn Ser Pro Gln Ser Ser Gly Thr Gly Arg Trp Arg Ser Gln Glu
 225 230 235 240
 Val Leu Glu Gly Ala Pro Pro Thr Leu Ala Gln Ala Pro Ile Gly Leu
 245 250 255
 Ser Pro His Pro Glu Gly Gly Pro Gly Ser Gly Arg Leu Gly Leu Arg
 260 265 270
 Arg Arg Ser Thr Ala Pro Asp Ile Pro Ser Leu Val Gly Glu Ala Pro
 275 280 285
 Gly Pro Glu Ser Gly Pro Glu Leu Glu Ala Asn Ala Leu Ser Val Ser
 290 295 300
 Val Pro Gly Pro Asn Pro Trp Gln Ala Gly Thr Glu Ala Val Val Leu
 305 310 315 320
 Arg Ala Gln Arg

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/28462

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 15/00, 12; C07K 14/435

US CL : 435/69.1, 320.1, 325; 530/350; 536/23.1, 23.5

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 320.1, 325; 530/350; 536/23.1, 23.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A, P	Genbank Accession No. AC007395, 30 September 2000 (30.09.00), see in particular nucleotides 123581 through 122421.	1-7



Further documents are listed in the continuation of Box C.



See patent family annex.

<p>* Special categories of cited documents:</p>		
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family	
"P" document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

30 October 2001 (30.10.2001)

Date of mailing of the international search report

15 JAN 2002

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703)305-3230

Authorized officer

Marianne P. Allen

Telephone No. 703-308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/28462

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7 with respect to SEQ ID NOS: 1 and 45

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/28462

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Claims 1-7 reference SEQ ID NOS. listed in Table 1 on page 24 of the description. Each nucleotide and corresponding amino acid sequence pair in Table 1 forms an inventive concept. Thus, with respect to claims 1-7, SEQ ID NOS: 1 and 45 form the first inventive concept, SEQ ID NOS: 2 and 46 form the second inventive concept, and so forth. There are a total of 44 inventions encompassed by the claims. The different sequence pairs have no obvious special technical feature in common as they appear to be structurally unrelated sequences.

As such, claims 1-7 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features.